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Nucleic Acids, Proteins, and Antibodies

Statement under 37 C.F.R. § 1.77(b)(4)

[1] This application refers to a "Sequence Listing" listed below, which is provided as an electronic document on two identical compact discs (CD-R), labeled "Copy 1" and "Copy 2." These compact discs each contain the following files, which are hereby incorporated in their entirety herein:

| Document | File Name | Size in bytes | Date of Creation |
|-------------------------------|-------------------|---------------|------------------|
| Sequence Listing | PTZ32_seqList.txt | 3,411,250 | 01/15/2001 |
| V Viewer Setup File | SetupDLL.exe | 695,808 | 12/19/2000 |
| V Viewer Help File Controller | v.cnt | 7,984 | 01/05/2001 |
| V Viewer Program File | v.exe | 753,664 | 12/19/2000 |
| V Viewer Help File | v.hlp | 447,766 | 01/05/2001 |

[2] The Sequence Listing may be viewed on an IBM-PC machine running the MS-Windows operating system by using the V viewer software, licensed by HGS, Inc., included on the compact discs (see World Wide Web URL: <http://www.fileviewer.com>).

Field of the Invention

[3] The present invention relates to novel proteins. More specifically, isolated nucleic acid molecules are provided encoding novel polypeptides. Novel polypeptides and antibodies that bind to these polypeptides are provided. Also provided are vectors, host cells, and recombinant and synthetic methods for producing human polynucleotides and/or polypeptides, and antibodies. The invention further relates to diagnostic and therapeutic

methods useful for diagnosing, treating, preventing and/or prognosing disorders related to these novel polypeptides. The invention further relates to screening methods for identifying agonists and antagonists of polynucleotides and polypeptides of the invention. The present invention further relates to methods and/or compositions for inhibiting or enhancing the production and function of the polypeptides of the present invention.

Background of the Invention

[4] One of the most critical tasks a cell must perform is to respond to cues from its environment, i.e., extracellular signals. Some of the most important extracellular signals come from other cells. The ability for cells to be able to send and receive signals from one another is of paramount importance in multicellular organisms because it allows individual cells within a body to become highly specialized and yet work in a coordinated fashion with other cells of the body. Cellular signaling mechanisms regulate a variety of cellular processes such as, for example, proliferation, differentiation, survival, movement, and secretion. Defects in cellular signaling can lead to a number of diseases and disorders such as cancers, immune system disorders and nervous system disorders. For more expansive reviews on this subject, please refer to Hunter, *Cell* 100:113-127 and Chapter 15 of *Molecular Biology of the Cell*, Third Edition, edited by Alberts et al. (1994), which are herein incorporated by reference in their entirety.

[5] Signal transduction requires molecules that serve as the extracellular signaling molecules as well as a set of receptors that "receive" the signal. Frequently, an additional set of proteins is necessary in order for the cell to translate the signal it has received into an appropriate response via the activation or inhibition of a particular set of genes or proteins. The signaling molecules, the receptor proteins, and the molecules that relay the signal between the receptor and the final effector molecules collectively form what are known as signal transduction pathways.

[6] To date, several common types of signal transduction pathways have been identified. One way to classify a signal transduction pathway is based on the class of receptor protein it utilizes. Two well known classes of receptor proteins are G-protein coupled receptors and enzyme-linked receptors. This latter class of enzyme-linked receptors includes receptor tyrosine kinases, tyrosine kinase associated receptors, receptor serine/threonine kinases, receptor tyrosine phosphatases, and receptor guanylyl cyclases.

Signal Transduction through G-protein Coupled Receptors

[7] G protein coupled receptors are the largest family of cell surface receptors. They are seven-pass transmembrane receptors which activate trimeric G proteins (G proteins) upon ligand binding. G proteins are GTPases composed of three subunits: alpha, beta and gamma. G proteins function as molecular switches existing in two states: an active GTP bound state and an inactive GDP bound state. Ligand binding to G protein coupled receptors induce inactive G proteins to release GDP allowing GTP to bind in its place. Binding of GTP to a G protein causes the alpha subunit to dissociate from the beta and gamma subunits which remain associated with one another. Eventually, the GTPase activity of the alpha subunit results in hydrolysis of the bound GTP molecule to GDP, thus inactivating the G protein.

[8] There are several types of G proteins that have been classified based upon their function. Stimulatory G proteins (G_s) are involved in adenylate cyclase activation; inhibitory G proteins (G_i) function to inhibit the activity of adenylate cyclase. Yet another type of G protein, G_q proteins, functions in the activation of phosphoinositide-specific phospholipase C enzyme.

[9] Activation of adenylate cyclase by an activated G_s protein results in the production of the cyclic nucleotide, cyclic AMP (cAMP). cAMP mediates its effects mostly through its activation of cAMP dependent kinase (A-kinase), a serine/threonine kinase. Activation of A-kinase helps to further relay the signal from the G protein coupled receptor to the target proteins. In muscle cells, for instance, activation of A-kinase following adrenaline signaling ultimately results in the activation of an enzyme, glycogen phosphorylase, which catalyzes the release of glucose molecules which can be used to produce energy from glycogen. In other instances, activated A-kinase translocates to the nucleus where it phosphorylates the cAMP response element binding (CREB) protein, which when phosphorylated, acts as a transcription factor to stimulate the expression of genes that have cAMP response elements (CRE) sequences in their regulatory regions.

[10] G_q proteins, when activated, activate the enzyme phospholipase C-beta which hydrolyzes PI 4,5-bisphosphate (PIP_2) producing inositol triphosphate (IP_3) and diacylglycerol (DAG). IP_3 functions as a second messenger that causes the release of Ca^{2+} from intracellular stores. Released calcium then binds to Ca^{2+} binding proteins such as calmodulin, which in its calcium bound state, is able to activate Ca^{2+} /calmodulin dependent protein kinases (CaM-kinases). Activated CaM kinases then continue to relay the signal to

more downstream molecules in the signal transduction pathway. The other product produced by phospholipase C-beta, DAG, functions to activate the serine/threonine kinase known as protein kinase C (PKC). Activated PKC phosphorylates target proteins depending on the cell type, and in many cells these phosphorylation events lead to the increased transcription of specific genes. The highest concentrations of protein kinase C are found in the brain where PKC phosphorylates ion channels in nerve cells thereby altering their excitability. PKC activation can be induced by treating cells with phorbol esters which are able to cross the plasma membrane, bind to, and activate PKC directly.

Signal Transduction through Receptor Tyrosine Kinases

[11] The receptor protein tyrosine kinases (RPTKs) are some of the most well studied receptors, and the signaling cascades they initiate demonstrate two of the fundamental concepts in signal transduction: the regulation of protein phosphorylation and the recruitment of proteins into a signaling cascade via protein-protein interaction domains.

[12] Binding of the cognate ligand to a RPTK, such as epidermal growth factor (EGF) binding to the epidermal growth factor receptor (EGFR), induces RPTKs to dimerize and cross-phosphorylate each other on multiple tyrosine residues. The phosphorylated receptor dimer is the activated form of the receptor.

[13] The phosphorylated tyrosines on activated RPTKs are then recognized/bound by other components of the signal transduction pathway. One of the important discoveries in the field of signal transduction was the recognition of conserved domains which allow for protein-protein interactions in signaling pathways. The most prevalent binding domain that recognizes phosphotyrosine (P-Tyr) residues is known as the SH2 domain (for Src homology region 2, named after the Src protein in which the SH2 domain was first discovered). Another domain that recognizes P-Tyr residues is called the P-Tyr binding domain (PTB). The discovery of the SH2 domain was quickly followed by the discovery of several other protein-protein interaction domains involved in signal transduction and by the realization that most of these domains are modular in nature, meaning these domains fold independently – a most convenient feature for protein engineering. To date, more than 100 such protein interaction domains involved in signaling have been defined via comparative sequence analysis. Most of these domains recognize short linear sequences (approximately 4-10 amino acid residues in length), in some cases requiring phosphorylation of specific residues within the sequence allowing for inducible association. A convenient web based database, with

links to abstracts of papers characterizing these domains can be found at <http://smart.EMBL-Heidelberg.de>.

[14] Proteins containing SH2 and PTB domains translocate to the plasma membrane where they associate with the activated RPTKs which, in turn, activates them through phosphorylation. By way of example, activation of the platelet derived growth factor receptor (PDGFR) results in the autophosphorylation of tyrosine residues in the cytoplasmic tail of the PDGFR. These P-Tyr residues then serve as the binding sites for other proteins, such as a GTPase (discussed in more detail below), phospholipase C-gamma, and the regulatory subunit of PI-3-kinase, which are each able to recognize the P-Tyr residues in PDGFR via SH2 domains. The interaction of these proteins with the activated PDGFR results in the translocation of these proteins to the plasma membranes where they have their substrates and the PDGFR mediated activation of these proteins via phosphorylation.

[15] In the previous example, each of the proteins recruited to the activated RPTK via their SH2 domains also had catalytic activities that allowed them to propagate a signal. There are proteins involved in signal transduction, however, which have no ability in and of themselves to propagate a signal. Instead, these proteins, known as adaptor proteins, serve to couple activated RPTKs to other components of the signal transduction pathway which do have the capacity to propagate the signal. One such adaptor protein is known as Grb2. It contains one SH2 domain and two SH3 domains (another Src homology domain that mediates protein interactions). Grb 2 is constitutively associated with Sos protein, a guanine nucleotide releasing protein (GNRP), via its SH3 domain. Thus, when Grb2 associates with an activated receptor via its SH2 domain, it also brings Sos into proximity with the RPTK which activates the Sos protein via phosphorylation.

[16] GNRP proteins, such as Sos, are one of two types of proteins that help regulate the activity of proteins belonging to the Ras superfamily of monomeric GTPases. Ras proteins are proteins that are associated with the cytoplasmic side of the plasma membrane and help relay signals from RPTK to the nucleus to stimulate cell proliferation or differentiation. Ras proteins exist in two states, an inactive state in which ras is bound to GDP and an active state in which ras is bound to GTP. Activated GNRP proteins promote the exchange of bound GDP for GTP on ras proteins, thereby activating ras. Ras, itself, is a GTPase that hydrolyzes GTP to GDP, and would therefore tend to inactivate itself over time. However, ras is an inefficient GTPase, so the inactivation of ras is enhanced by GTPase activating proteins (GAPs) which increase the rate of hydrolysis of GTP by ras.

[17] Activated Ras kinases then act to activate more downstream signaling events, including activation of the mitogen-activated protein kinase (MAPK) pathway which is a cascade of serine/threonine kinases. Ras binds to and activates a MAPK kinase kinase (MAPKKK, such as Raf-1, for example), which in turn activates a MAPK kinase (MAPKK) via phosphorylation, which in turn activates a MAPK. MAPKs relay signals downstream by phosphorylating various proteins in the cell including other kinases and/or regulatory proteins in the cell. For instance, an activated MAPK can enter the nucleus and help to initiate transcription of genes that must be expressed in order for the cell to respond to the extracellular signal, such as genes required for DNA replication in response to the extracellular proliferation signal.

[18] Another class of signaling receptors, receptor serine/threonine kinases (RSK) has recently been identified. An example of an RSK is the TGF-beta receptor. Additionally, it has also been recently recognized that there are modular binding domains that recognize phosphoserine/phosphothreonine (P-Ser/P-Thr) residues. For instance, 14-3-3 domains recognize phosphoserines in specific amino acid contexts [RSX(P-Ser)XP] or [R(Y/F)X(P-Ser)XP] and may function in the assembly of signaling complexes. Other residues such as histidine and arginine can also be phosphorylated, and it is possible that additional kinases which phosphorylate these residues, or protein domains that bind phosphohistidine or phosphoarginine will be discovered.

Signaling Via Intracellular Receptors

[19] Some extracellular signals do not have cell surface receptors such as G protein coupled receptors or receptor tyrosine kinases. Instead, these extracellular signals are able to traverse the plasma membrane and interact with their receptors in the cytoplasm. Examples of such signals are the steroid hormones and the gas nitrous oxide (NO). The steroid hormone receptors, once bound by their ligand, are generally able to translocate to the nucleus where they bind regulatory DNA elements that control the gene expression of specific genes. NO gas, on the other hand, generally enters a cell and reacts with iron in the active site of the enzyme guanylate cyclase, stimulating it to produce cyclic GMP (cGMP). cGMP acts as a second messenger (similar to the way cAMP functions) and can stimulate further downstream signaling by binding to other proteins.

Terminating Signal Transduction

[20] As the effects of signal transduction are transient, there must also be mechanisms for terminating signal cascades. For example, G proteins are self-inactivating, and there are a set of proteins, GAPs, that are devoted to increasing the rate of hydrolysis of bound GTP by ras proteins. Cyclic nucleotide second messengers such as cAMP and cGMP are hydrolyzed by phosphodiesterases. In the case of kinases, there generally exist a set of complementary phosphatases that function to dephosphorylate phosphorylated residues, thereby bringing the signaling event to a close.

Signal Transduction Pathway Components and Disease

[21] Because signal transduction is involved in the regulation of so many cellular processes, including proliferation, differentiation, survival, and apoptosis, it is not surprising that defects in cellular signal transduction pathway components lead to a number of diseases and disorders, especially cancers. For a review on Signal transduction pathway components and diseases, see Hunter, Philosophical Transactions of the Royal Society of London Series B 353:583-605 (1998) which is herein incorporated by reference in its entirety. For instance, approximately 30% of human cancers have mutations in a ras gene, and at least 18 tyrosine kinases have been identified as oncogenes in either acutely transforming retroviruses or in human tumors, such as for example, Src. And more than 95% of chronic myelogenous leukemias express an activated form of the c-Abl non-receptor tyrosine kinases.

[22] Mutations in signaling pathways are also implicated in a plethora of other diseases. Mutation in Bruton's tyrosine kinase leads to X-linked agammaglobulinemia. Inactivation of ZAP70 or JAK3 leads to a severe combined immunodeficiency disease. Coffin-Lowry syndrome occurs when the X-linked Rsk2 protein serine kinase gene is inactivated. Myotonic dystrophy occurs when expression of the myotonic dystrophy serine kinase gene is decreased. Overexpression of the aurora2 serine kinase is implicated in colon carcinoma.

[23] The malfunction of signal transduction pathway components, particularly kinases, in diseases indicate that these genes are good targets for drugs/pharmaceuticals that either inhibit or activate their function. In fact, some such drugs have been developed and are already in use or in clinical trials. For instance, an inhibitor of cyclin dependent kinase 2 (cdk2), a kinase important in regulating cellular proliferation, is in clinical trials for cancer treatment, as are inhibitors of epidermal growth factor receptor tyrosine kinases and vascular endothelial growth factor receptor (VEGFR) tyrosine kinases. Inhibition of VEGFR activity

reduces or eliminates the vascularization of tumors directed by VEGFR. An antagonistic monoclonal antibody, herceptin, against the erbB2 receptor tyrosine kinase is being used in breast cancer therapies to treat breast cancers where ErbB2 is overexpressed.

[24] Thus there exists a clear need for identifying and exploiting novel signal transduction pathway component polynucleotides and polypeptides. Although structurally related, such proteins may possess diverse and multifaceted functions in a variety of cell and tissue types. The inventive purified signal transduction pathway component polypeptides are research tools useful for the identification, characterization and purification of additional proteins involved in signal transduction. Furthermore, the identification of new signal transduction pathway component polynucleotides and polypeptides permits the development of a range of derivatives, agonists and antagonists at the nucleic acid and protein levels which in turn have applications in the treatment and diagnosis of a range of conditions such as, for example, cancer and other proliferative disorders (e.g., chronic myelogenous leukemia), immunological disorders (e.g., severe combined immunodeficiency and X-linked agammaglobulinemia), and nervous system disorders (Coffin-Lowry Syndrome), amongst other conditions.

Summary of the Invention

[25] The present invention relates to novel proteins. More specifically, isolated nucleic acid molecules are provided encoding novel polypeptides. Novel polypeptides and antibodies that bind to these polypeptides are provided. Also provided are vectors, host cells, and recombinant and synthetic methods for producing human polynucleotides and/or polypeptides, and antibodies. The invention further relates to diagnostic and therapeutic methods useful for diagnosing, treating, preventing and/or prognosing disorders related to these novel polypeptides. The invention further relates to screening methods for identifying agonists and antagonists of polynucleotides and polypeptides of the invention. The present invention further relates to methods and/or compositions for inhibiting or enhancing the production and function of the polypeptides of the present invention.

Detailed Description

Tables

[26] Table 1A summarizes some of the polynucleotides encompassed by the invention (including cDNA clones related to the sequences (Clone ID NO:Z), contig sequences (contig identifier (Contig ID:)) and contig nucleotide sequence identifier (SEQ ID NO:X)) and further summarizes certain characteristics of these polynucleotides and the polypeptides encoded thereby. The first column provides the gene number in the application for each clone identifier. The second column provides a unique clone identifier, "Clone ID NO:Z", for a cDNA clone related to each contig sequence disclosed in Table 1A. The third column provides a unique contig identifier, "Contig ID:" for each of the contig sequences disclosed in Table 1A. The fourth column provides the sequence identifier, "SEQ ID NO:X", for each of the contig sequences disclosed in Table 1A. The fifth column, "ORF (From-To)", provides the location (i.e., nucleotide position numbers) within the polynucleotide sequence of SEQ ID NO:X that delineate the preferred open reading frame (ORF) that encodes the amino acid sequence shown in the sequence listing and referenced in Table 1A as SEQ ID NO:Y (column 6). Column 7 lists residues comprising predicted epitopes contained in the polypeptides encoded by each of the preferred ORFs (SEQ ID NO:Y). Identification of potential immunogenic regions was performed according to the method of Jameson and Wolf (CABIOS, 4; 181-186 (1988)); specifically, the Genetics Computer Group (GCG) implementation of this algorithm, embodied in the program PEPTIDESTRUCTURE (Wisconsin Package v10.0, Genetics Computer Group (GCG), Madison, Wisc.). This method returns a measure of the probability that a given residue is found on the surface of the protein. Regions where the antigenic index score is greater than 0.9 over at least 6 amino acids are indicated in Table 1A as "Predicted Epitopes". In particular embodiments, polypeptides of the invention comprise, or alternatively consist of, one, two, three, four, five or more of the predicted epitopes described in Table 1A. It will be appreciated that depending on the analytical criteria used to predict antigenic determinants, the exact address of the determinant may vary slightly. Column 8, "Tissue Distribution" shows the expression profile of tissue, cells, and/or cell line libraries which express the polynucleotides of the invention. The first number in column 8 (preceding the colon), represents the tissue/cell source identifier code corresponding to the key provided in Table 4. Expression of these polynucleotides was not observed in the other tissues and/or cell libraries tested. For those identifier codes in which the first two letters are not "AR", the second number in column 8 (following the colon), represents the number of times a sequence corresponding to the reference polynucleotide sequence (e.g., SEQ ID NO:X) was identified in the tissue/cell source. Those tissue/cell

source identifier codes in which the first two letters are "AR" designate information generated using DNA array technology. Utilizing this technology, cDNAs were amplified by PCR and then transferred, in duplicate, onto the array. Gene expression was assayed through hybridization of first strand cDNA probes to the DNA array. cDNA probes were generated from total RNA extracted from a variety of different tissues and cell lines. Probe synthesis was performed in the presence of ³³P dCTP, using oligo(dT) to prime reverse transcription. After hybridization, high stringency washing conditions were employed to remove non-specific hybrids from the array. The remaining signal, emanating from each gene target, was measured using a Phosphorimager. Gene expression was reported as Phosphor Stimulating Luminescence (PSL) which reflects the level of phosphor signal generated from the probe hybridized to each of the gene targets represented on the array. A local background signal subtraction was performed before the total signal generated from each array was used to normalize gene expression between the different hybridizations. The value presented after "[array code]:" represents the mean of the duplicate values, following background subtraction and probe normalization. One of skill in the art could routinely use this information to identify normal and/or diseased tissue(s) which show a predominant expression pattern of the corresponding polynucleotide of the invention or to identify polynucleotides which show predominant and/or specific tissue and/or cell expression. Column 9 provides the chromosomal location of polynucleotides corresponding to SEQ ID NO:X. Chromosomal location was determined by finding exact matches to EST and cDNA sequences contained in the NCBI (National Center for Biotechnology Information) UniGene database. Given a presumptive chromosomal location, disease locus association was determined by comparison with the Morbid Map, derived from Online Mendelian Inheritance in Man (Online Mendelian Inheritance in Man, OMIM™. McKusick-Nathans Institute for Genetic Medicine, Johns Hopkins University (Baltimore, MD) and National Center for Biotechnology Information, National Library of Medicine (Bethesda, MD) 2000. World Wide Web URL: <http://www.ncbi.nlm.nih.gov/omim/>). If the putative chromosomal location of the Query overlaps with the chromosomal location of a Morbid Map entry, an OMIM identification number is disclosed in column 10 labeled "OMIM Disease Reference(s)". A key to the OMIM reference identification numbers is provided in Table 5.

[27] Table 1B summarizes additional polynucleotides encompassed by the invention (including cDNA clones related to the sequences (Clone ID NO:Z), contig sequences (contig identifier (Contig ID:) contig nucleotide sequence identifiers (SEQ ID NO:X)), and genomic

sequences (SEQ ID NO:B). The first column provides a unique clone identifier, "Clone ID NO:Z", for a cDNA clone related to each contig sequence. The second column provides the sequence identifier, "SEQ ID NO:X", for each contig sequence. The third column provides a unique contig identifier, "Contig ID:" for each contig sequence. The fourth column, provides a BAC identifier "BAC ID NO:A" for the BAC clone referenced in the corresponding row of the table. The fifth column provides the nucleotide sequence identifier, "SEQ ID NO:B" for a fragment of the BAC clone identified in column four of the corresponding row of the table. The sixth column, "Exon From-To", provides the location (i.e., nucleotide position numbers) within the polynucleotide sequence of SEQ ID NO:B which delineate certain polynucleotides of the invention that are also exemplary members of polynucleotide sequences that encode polypeptides of the invention (e.g., polypeptides containing amino acid sequences encoded by the polynucleotide sequences delineated in column six, and fragments and variants thereof).

[28] Table 2 summarizes homology and features of some of the polypeptides of the invention. The first column provides a unique clone identifier, "Clone ID NO:Z", corresponding to a cDNA clone disclosed in Table 1A. The second column provides the unique contig identifier, "Contig ID:" corresponding to contigs in Table 1A and allowing for correlation with the information in Table 1A. The third column provides the sequence identifier, "SEQ ID NO:X", for the contig polynucleotide sequence. The fourth column provides the analysis method by which the homology/identity disclosed in the Table was determined. Comparisons were made between polypeptides encoded by the polynucleotides of the invention and either a non-redundant protein database (herein referred to as "NR"), or a database of protein families (herein referred to as "PFAM") as further described below. The fifth column provides a description of the PFAM/NR hit having a significant match to a polypeptide of the invention. Column six provides the accession number of the PFAM/NR hit disclosed in the fifth column. Column seven, "Score/Percent Identity", provides a quality score or the percent identity, of the hit disclosed in columns five and six. Columns 8 and 9, "NT From" and "NT To" respectively, delineate the polynucleotides in "SEQ ID NO:X" that encode a polypeptide having a significant match to the PFAM/NR database as disclosed in the fifth and sixth columns. In specific embodiments polypeptides of the invention comprise, or alternatively consist of, an amino acid sequence encoded by a polynucleotide in SEQ ID NO:X as delineated in columns 8 and 9, or fragments or variants thereof.

[29] Table 3 provides polynucleotide sequences that may be disclaimed according to

certain embodiments of the invention. The first column provides a unique clone identifier, "Clone ID", for a cDNA clone related to contig sequences disclosed in Table 1A. The second column provides the sequence identifier, "SEQ ID NO:X", for contig sequences disclosed in Table 1A. The third column provides the unique contig identifier, "Contig ID:", for contigs disclosed in Table 1A. The fourth column provides a unique integer 'a' where 'a' is any integer between 1 and the final nucleotide minus 15 of SEQ ID NO:X, and the fifth column provides a unique integer 'b' where 'b' is any integer between 15 and the final nucleotide of SEQ ID NO:X, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:X, and where b is greater than or equal to a + 14. For each of the polynucleotides shown as SEQ ID NO:X, the uniquely defined integers can be substituted into the general formula of a-b, and used to describe polynucleotides which may be preferably excluded from the invention. In certain embodiments, preferably excluded from the invention are at least one, two, three, four, five, ten, or more of the polynucleotide sequence(s) having the accession number(s) disclosed in the sixth column of this Table (including for example, published sequence in connection with a particular BAC clone). In further embodiments, preferably excluded from the invention are the specific polynucleotide sequence(s) contained in the clones corresponding to at least one, two, three, four, five, ten, or more of the available material having the accession numbers identified in the sixth column of this Table (including for example, the actual sequence contained in an identified BAC clone).

[30] Table 4 provides a key to the tissue/cell source identifier code disclosed in Table 1A, column 8. Column 1 provides the tissue/cell source identifier code disclosed in Table 1A, Column 8. Columns 2-5 provide a description of the tissue or cell source. Codes corresponding to diseased tissues are indicated in column 6 with the word "disease". The use of the word "disease" in column 6 is non-limiting. The tissue or cell source may be specific (e.g. a neoplasm), or may be disease-associated (e.g., a tissue sample from a normal portion of a diseased organ). Furthermore, tissues and/or cells lacking the "disease" designation may still be derived from sources directly or indirectly involved in a disease state or disorder, and therefore may have a further utility in that disease state or disorder. In numerous cases where the tissue/cell source is a library, column 7 identifies the vector used to generate the library.

[31] Table 5 provides a key to the OMIM reference identification numbers disclosed in Table 1A, column 10. OMIM reference identification numbers (Column 1) were derived from Online Mendelian Inheritance in Man (Online Mendelian Inheritance in Man, OMIM.

McKusick-Nathans Institute for Genetic Medicine, Johns Hopkins University (Baltimore, MD) and National Center for Biotechnology Information, National Library of Medicine, (Bethesda, MD) 2000. World Wide Web URL: <http://www.ncbi.nlm.nih.gov/omim/>). Column 2 provides diseases associated with the cytologic band disclosed in Table 1A, column 9, as determined using the Morbid Map database.

[32] Table 6 summarizes ATCC Deposits, Deposit dates, and ATCC designation numbers of deposits made with the ATCC in connection with the present application.

[33] Table 7 shows the cDNA libraries sequenced, and ATCC designation numbers and vector information relating to these cDNA libraries.

[34] Table 8 provides a physical characterization of clones encompassed by the invention. The first column provides the unique clone identifier, "Clone ID NO:Z", for certain cDNA clones of the invention, as described in Table 1A. The second column provides the size of the cDNA insert contained in the corresponding cDNA clone.

Definitions

[35] The following definitions are provided to facilitate understanding of certain terms used throughout this specification.

[36] In the present invention, "isolated" refers to material removed from its original environment (e.g., the natural environment if it is naturally occurring), and thus is altered "by the hand of man" from its natural state. For example, an isolated polynucleotide could be part of a vector or a composition of matter, or could be contained within a cell, and still be "isolated" because that vector, composition of matter, or particular cell is not the original environment of the polynucleotide. The term "isolated" does not refer to genomic or cDNA libraries, whole cell total or mRNA preparations, genomic DNA preparations (including those separated by electrophoresis and transferred onto blots), sheared whole cell genomic DNA preparations or other compositions where the art demonstrates no distinguishing features of the polynucleotide/sequences of the present invention.

[37] As used herein, a "polynucleotide" refers to a molecule having a nucleic acid sequence encoding SEQ ID NO:Y or a fragment or variant thereof; a nucleic acid sequence contained in SEQ ID NO:X (as described in column 3 of Table 1A) or the complement thereof; a cDNA sequence contained in Clone ID NO:Z (as described in column 2 of Table 1A and contained within a library deposited with the ATCC); a nucleotide sequence encoding

the polypeptide encoded by a nucleotide sequence in SEQ ID NO:B as defined in column 6 of Table 1B or a fragment or variant thereof; or a nucleotide coding sequence in SEQ ID NO:B as defined in column 6 of Table 1B or the complement thereof. For example, the polynucleotide can contain the nucleotide sequence of the full length cDNA sequence, including the 5' and 3' untranslated sequences, the coding region, as well as fragments, epitopes, domains, and variants of the nucleic acid sequence. Moreover, as used herein, a "polypeptide" refers to a molecule having an amino acid sequence encoded by a polynucleotide of the invention as broadly defined (obviously excluding poly-Phenylalanine or poly-Lysine peptide sequences which result from translation of a polyA tail of a sequence corresponding to a cDNA).

[38] In the present invention, "SEQ ID NO:X" was often generated by overlapping sequences contained in multiple clones (contig analysis). A representative clone containing all or most of the sequence for SEQ ID NO:X is deposited at Human Genome Sciences, Inc. (HGS) in a catalogued and archived library. As shown, for example, in column 2 of Table 1A, each clone is identified by a cDNA Clone ID (identifier generally referred to herein as Clone ID NO:Z). Each Clone ID is unique to an individual clone and the Clone ID is all the information needed to retrieve a given clone from the HGS library. Furthermore, certain clones disclosed in this application have been deposited with the ATCC on October 5, 2000, having the ATCC designation numbers PTA 2574 and PTA 2575; and on January 5, 2001, having the depositor reference numbers TS-1, TS-2, AC-1, and AC-2. In addition to the individual cDNA clone deposits, most of the cDNA libraries from which the clones were derived were deposited at the American Type Culture Collection (hereinafter "ATCC"). Table 7 provides a list of the deposited cDNA libraries. One can use the Clone ID NO:Z to determine the library source by reference to Tables 6 and 7. Table 7 lists the deposited cDNA libraries by name and links each library to an ATCC Deposit. Library names contain four characters, for example, "HTWE." The name of a cDNA clone (Clone ID) isolated from that library begins with the same four characters, for example "HTWEP07". As mentioned below, Table 1A correlates the Clone ID names with SEQ ID NO:X. Thus, starting with an SEQ ID NO:X, one can use Tables 1, 6 and 7 to determine the corresponding Clone ID, which library it came from and which ATCC deposit the library is contained in. Furthermore, it is possible to retrieve a given cDNA clone from the source library by techniques known in the art and described elsewhere herein. The ATCC is located at 10801 University Boulevard, Manassas, Virginia 20110-2209, USA. The ATCC deposits were made pursuant to the terms

of the Budapest Treaty on the international recognition of the deposit of microorganisms for the purposes of patent procedure.

[39] In specific embodiments, the polynucleotides of the invention are at least 15, at least 30, at least 50, at least 100, at least 125, at least 500, or at least 1000 continuous nucleotides but are less than or equal to 300 kb, 200 kb, 100 kb, 50 kb, 15 kb, 10 kb, 7.5kb, 5 kb, 2.5 kb, 2.0 kb, or 1 kb, in length. In a further embodiment, polynucleotides of the invention comprise a portion of the coding sequences, as disclosed herein, but do not comprise all or a portion of any intron. In another embodiment, the polynucleotides comprising coding sequences do not contain coding sequences of a genomic flanking gene (i.e., 5' or 3' to the gene of interest in the genome). In other embodiments, the polynucleotides of the invention do not contain the coding sequence of more than 1000, 500, 250, 100, 50, 25, 20, 15, 10, 5, 4, 3, 2, or 1 genomic flanking gene(s).

[40] A "polynucleotide" of the present invention also includes those polynucleotides capable of hybridizing, under stringent hybridization conditions, to sequences contained in SEQ ID NO:X, or the complement thereof (e.g., the complement of any one, two, three, four, or more of the polynucleotide fragments described herein), the polynucleotide sequence delineated in columns 8 and 9 of Table 2 or the complement thereof, and/or cDNA sequences contained in Clone ID NO:Z (e.g., the complement of any one, two, three, four, or more of the polynucleotide fragments, or the cDNA clone within the pool of cDNA clones deposited with the ATCC, described herein), and/or the polynucleotide sequence delineated in column 6 of Table 1B or the complement thereof. "Stringent hybridization conditions" refers to an overnight incubation at 42 degree C in a solution comprising 50% formamide, 5x SSC (750 mM NaCl, 75 mM trisodium citrate), 50 mM sodium phosphate (pH 7.6), 5x Denhardt's solution, 10% dextran sulfate, and 20 µg/ml denatured, sheared salmon sperm DNA, followed by washing the filters in 0.1x SSC at about 65 degree C.

[41] Also contemplated are nucleic acid molecules that hybridize to the polynucleotides of the present invention at lower stringency hybridization conditions. Changes in the stringency of hybridization and signal detection are primarily accomplished through the manipulation of formamide concentration (lower percentages of formamide result in lowered stringency); salt conditions, or temperature. For example, lower stringency conditions include an overnight incubation at 37 degree C in a solution comprising 6X SSPE (20X SSPE = 3M NaCl; 0.2M NaH₂PO₄; 0.02M EDTA, pH 7.4), 0.5% SDS, 30% formamide, 100 ug/ml salmon sperm blocking DNA; followed by washes at 50 degree C with 1XSSPE, 0.1% SDS.

In addition, to achieve even lower stringency, washes performed following stringent hybridization can be done at higher salt concentrations (e.g. 5X SSC).

[42] Note that variations in the above conditions may be accomplished through the inclusion and/or substitution of alternate blocking reagents used to suppress background in hybridization experiments. Typical blocking reagents include Denhardt's reagent, BLOTTO, heparin, denatured salmon sperm DNA, and commercially available proprietary formulations. The inclusion of specific blocking reagents may require modification of the hybridization conditions described above, due to problems with compatibility.

[43] Of course, a polynucleotide which hybridizes only to polyA⁺ sequences (such as any 3' terminal polyA⁺ tract of a cDNA shown in the sequence listing), or to a complementary stretch of T (or U) residues, would not be included in the definition of "polynucleotide," since such a polynucleotide would hybridize to any nucleic acid molecule containing a poly (A) stretch or the complement thereof (e.g., practically any double-stranded cDNA clone generated using oligo dT as a primer).

[44] The polynucleotide of the present invention can be composed of any polyribonucleotide or polydeoxribonucleotide, which may be unmodified RNA or DNA or modified RNA or DNA. For example, polynucleotides can be composed of single- and double-stranded DNA, DNA that is a mixture of single- and double-stranded regions, single- and double-stranded RNA, and RNA that is mixture of single- and double-stranded regions, hybrid molecules comprising DNA and RNA that may be single-stranded or, more typically, double-stranded or a mixture of single- and double-stranded regions. In addition, the polynucleotide can be composed of triple-stranded regions comprising RNA or DNA or both RNA and DNA. A polynucleotide may also contain one or more modified bases or DNA or RNA backbones modified for stability or for other reasons. "Modified" bases include, for example, tritylated bases and unusual bases such as inosine. A variety of modifications can be made to DNA and RNA; thus, "polynucleotide" embraces chemically, enzymatically, or metabolically modified forms.

[45] The polypeptide of the present invention can be composed of amino acids joined to each other by peptide bonds or modified peptide bonds, i.e., peptide isosteres, and may contain amino acids other than the 20 gene-encoded amino acids. The polypeptides may be modified by either natural processes, such as posttranslational processing, or by chemical modification techniques which are well known in the art. Such modifications are well described in basic texts and in more detailed monographs, as well as in a voluminous

research literature. Modifications can occur anywhere in a polypeptide, including the peptide backbone, the amino acid side-chains and the amino or carboxyl termini. It will be appreciated that the same type of modification may be present in the same or varying degrees at several sites in a given polypeptide. Also, a given polypeptide may contain many types of modifications. Polypeptides may be branched, for example, as a result of ubiquitination, and they may be cyclic, with or without branching. Cyclic, branched, and branched cyclic polypeptides may result from posttranslation natural processes or may be made by synthetic methods. Modifications include acetylation, acylation, ADP-ribosylation, amidation, covalent attachment of flavin, covalent attachment of a heme moiety, covalent attachment of a nucleotide or nucleotide derivative, covalent attachment of a lipid or lipid derivative, covalent attachment of phosphatidylinositol, cross-linking, cyclization, disulfide bond formation, demethylation, formation of covalent cross-links, formation of cysteine, formation of pyroglutamate, formylation, gamma-carboxylation, glycosylation, GPI anchor formation, hydroxylation, iodination, methylation, myristoylation, oxidation, pegylation, proteolytic processing, phosphorylation, prenylation, racemization, selenoylation, sulfation, transfer-RNA mediated addition of amino acids to proteins such as arginylation, and ubiquitination. (See, for instance, PROTEINS - STRUCTURE AND MOLECULAR PROPERTIES, 2nd Ed., T. E. Creighton, W. H. Freeman and Company, New York (1993); POSTTRANSLATIONAL COVALENT MODIFICATION OF PROTEINS, B. C. Johnson, Ed., Academic Press, New York, pgs. 1-12 (1983); Seifter et al., Meth. Enzymol. 182:626-646 (1990); Rattan et al., Ann. N.Y. Acad. Sci. 663:48-62 (1992)).

[46] "SEQ ID NO:X" refers to a polynucleotide sequence described, for example, in Tables 1A or 2, while "SEQ ID NO:Y" refers to a polypeptide sequence described in column 6 of Table 1A. SEQ ID NO:X is identified by an integer specified in column 4 of Table 1A. The polypeptide sequence SEQ ID NO:Y is a translated open reading frame (ORF) encoded by polynucleotide SEQ ID NO:X. "Clone ID NO:Z" refers to a cDNA clone described in column 2 of Table 1A.

[47] "A polypeptide having functional activity" refers to a polypeptide capable of displaying one or more known functional activities associated with a full-length (complete) protein. Such functional activities include, but are not limited to, biological activity, antigenicity [ability to bind (or compete with a polypeptide for binding) to an anti-polypeptide antibody], immunogenicity (ability to generate antibody which binds to a

specific polypeptide of the invention), ability to form multimers with polypeptides of the invention, and ability to bind to a receptor or ligand for a polypeptide.

[48] The polypeptides of the invention can be assayed for functional activity (e.g. biological activity) using or routinely modifying assays known in the art, as well as assays described herein. Specifically, one of skill in the art may routinely assay signal transduction pathway component polypeptides (including fragments and variants) of the invention for activity using assays as described in Examples 38, 39, 49, 52-57, 64 and 67.

[49] "A polypeptide having biological activity" refers to a polypeptide exhibiting activity similar to, but not necessarily identical to, an activity of a polypeptide of the present invention, including mature forms, as measured in a particular biological assay, with or without dose dependency. In the case where dose dependency does exist, it need not be identical to that of the polypeptide, but rather substantially similar to the dose-dependence in a given activity as compared to the polypeptide of the present invention (i.e., the candidate polypeptide will exhibit greater activity or not more than about 25-fold less and, preferably, not more than about tenfold less activity, and most preferably, not more than about three-fold less activity relative to the polypeptide of the present invention).

[50] Table 1A summarizes some of the polynucleotides encompassed by the invention (including contig sequences (SEQ ID NO:X) and clones (Clone ID NO:Z) and further summarizes certain characteristics of these polynucleotides and the polypeptides encoded thereby.

Polynucleotides and Polypeptides of the Invention

TABLE 1A

| Gene No: | Clone ID NO: Z | Contig ID: | SEQ ID NO: X | ORF (From-To) | AA SEQ ID NO: Y | Predicted Epitopes | Tissue Distribution Library code: count (see Table IV for Library Codes) | Cytologic Band | OMIM Disease Reference(s): |
|----------|-------------------|---------------|-----------------|------------------|--------------------------|---------------------|---|-------------------|----------------------------------|
| 1 | HDPTE21 | 1165861 | 11 | 33 - 1790 | 624 | Pro-16 to Gln-22, | AR051: 26, AR050: 22, AR054: 21, AR089: 1, AR061: 1 H0529: 4, L0770: 4, L0748: 4, L0749: 3, L0777: 3, S0036: 2, L0756: 2, S0360: 1, H0036: 1, H0318: 1, H0457: 1, H0051: 1, H0328: 1, H0644: 1, S0002: 1, L0761: 1, L0766: 1, L0804: 1, L0784: 1, H0521: 1 and L0759: 1. | | |
| | | | | | | Arg-34 to Asn-41, | | | |
| | | | | | | Arg-49 to Lys-55, | | | |
| | | | | | | Leu-156 to Thr-163, | | | |
| | | | | | | Glu-169 to Glu-174, | | | |
| | | | | | | Ser-198 to Glu-214, | | | |
| | | | | | | Glu-246 to Pro-252, | | | |
| | | | | | | Arg-260 to Ser-271, | | | |
| | | | | | | Val-286 to Gly-291, | | | |
| | | | | | | Ser-304 to Glu-335, | | | |
| | | | | | | Pro-436 to Pro-451, | | | |
| | | | | | | Ser-482 to Gly-487, | | | |
| | | | | | | Val-498 to Ser-505, | | | |
| | | | | | | Asp-564 to Lys-585. | | | |
| | | 887711 | 443 | 1 - 639 | 1056 | | | | |
| | | 901381 | 444 | 570 - 112 | 1057 | Gly-26 to Gly-32. | | | |
| 2 | H6EDR51 | 1197894 | 12 | 1 - 1935 | 625 | Glu-35 to Gln-44, | AR089: 1, AR061: 1 | | |
| | | | | | | Arg-70 to Val-77. | L0794: 11, L0777: 9. | | |

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|---|---------|---------|----|----------|-----|--------|-----|----------|------|--|---|--|--|
| 3 | HAPRA41 | 1154054 | 13 | 2 - 1276 | 626 | 930788 | 445 | 1 - 1248 | 1058 | Glu-26 to Gln-35, Arg-61 to Val-68, Ala-104 to Gly-114, Ser-119 to Phe-124, Gly-226 to His-233, Glu-240 to Leu-245, Pro-277 to Arg-283. | H0670: 1, S0378: 1, S0152: 1, H0696: 1, H0134: 1, L0779: 1, H0445: 1, H0542: 1 and H0423: 1. | | |
| | | | | | | | | | | Ser-5 to Arg-24, Trp-27 to Ala-32, Arg-48 to Gln-54, Lys-71 to Gln-79, Pro-93 to His-101, Lys-104 to Thr-110, Ser-119 to Gln-125, Val-141 to Pro-152, Leu-158 to Gly-171, Asn-183 to Ala-198, Gly-217 to Asp-233, Ser-244 to Asn-258, Lys-264 to Leu-269, Ser-310 to Gly-316. | AR061: 3, AR089: 2 L0777: 2, S0001: 1, S0222: 1, H0575: 1, H0618: 1, H0253: 1, H0266: 1, H0038: 1, H0616: 1, L0643: 1, L0352: 1 and L0758: 1. | | |

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| 4 | HBXBI07 | 926285 | 446 | 3 - 500 | 1059 | Thr-326 to Glu-333, Ser-396 to Pro-403, Leu-416 to Lys-425. | | | |
| | | | | | | Ser-3 to Arg-21, Trp-24 to Ala-29, Arg-45 to Gln-51, Lys-68 to Gln-76, Pro-90 to His-98, Lys-101 to Thr-107, Ser-116 to Gln-122. | | | |
| | | | | | | Ser-6 to Pro-14. | | | |
| 5 | HBXCM38 | 910086 | 15 | 402 - 1535 | 628 | Val-36 to Glu-43, Lys-66 to Glu-71. | | | |
| | | | | | | | | | |
| | | | | | | | | | |
| 4 | HBXBI07 | 1171958 | 14 | 1 - 228 | 627 | Ser-6 to Pro-14. | AR061: 1, AR089: 1 S0038: 1 | | |
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| | | | | | | | | | |
| 5 | HBXCM38 | 910086 | 15 | 402 - 1535 | 628 | Val-36 to Glu-43, Lys-66 to Glu-71. | AR061: 2, AR089: 1 L0439: 6, S0038: 3, L0803: 3, H0455: 2, L0769: 2, L0809: 2, L0741: 2, L0756: 2, S6024: 1, S0001: 1, H0663: 1, S0222: 1, H0441: 1, H0438: 1, H0036: 1, S0049: 1, H0309: 1, H0566: 1, H0024: 1, S0388: 1, S0051: 1, T0010: 1, H0059: 1, L0645: 1, | | |
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|---|---------|---------|----|----------|-----|--|--|--|--|--|--|
| | | | | | | | | L0774: 1, L0790: 1, L0663: 1, L0665: 1, H0345: 1, L0742: 1, L0748: 1, L0749: 1, H0707: 1, L0595: 1 and L0366: 1. | | | |
| 6 | HCE3E50 | 1227586 | 16 | 4 - 1650 | 629 | Pro-1 to Ser-10, Pro-24 to Ser-29, Pro-43 to Glu-61. | | AR061: 1, AR089: 1 H0521: 14, L0439: 6, L0754: 6, L0794: 4, L0748: 4, S0278: 3, L0766: 3, L0751: 3, L0747: 3, L0749: 3, H0556: 2, H0486: 2, H0250: 2, H0179: 2, H0271: 2, S0002: 2, S0426: 2, L0770: 2, L0769: 2, L0775: 2, L0659: 2, L0411: 1, S0134: 1, H0638: 1, S0418: 1, S0420: 1, S0354: 1, S0358: 1, S0360: 1, S0222: 1, H0613: 1, H0052: 1, H0051: 1, L0143: 1, L0455: 1, H0124: 1, H0090: 1, H0551: 1, | | | |

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|---|---------|--------|----|----------|-----|---|---|--|--|
| 9 | HDPLT89 | 962403 | 19 | 83 - 931 | 632 | <p>Tyr-73 to Gly-85, Ala-98 to Ala-104, Ser-115 to Asp-124, Gly-189 to Gly-194, Pro-199 to Leu-204, Ala-214 to Asp-225, Thr-260 to Gln-268, Pro-279 to Ser-284.</p> | <p>H0657: 2, H0553: 2, L0632: 2, L0748: 2, H0445: 2, L0605: 2, H0422: 2, H0265: 1, H0556: 1, S0114: 1, H0583: 1, H0650: 1, S0116: 1, H0341: 1, S0360: 1, H0676: 1, H0497: 1, H0486: 1, H0075: 1, H0581: 1, H0421: 1, S0388: 1, H0271: 1, H0031: 1, H0090: 1, H0591: 1, H0038: 1, L0638: 1, L0667: 1, L0363: 1, L0774: 1, L0775: 1, L0658: 1, L0659: 1, L0809: 1, L0647: 1, L0790: 1, H0701: 1, H0658: 1, H0555: 1, L0779: 1, L0777: 1, L0731: 1 and H0423: 1.</p> | | |
| | | | | | | <p>Lys-13 to Gly-28, Arg-64 to Gly-71, Pro-131 to Glu-137, Gln-152 to Asp-159,</p> | <p>AR054: 57, AR051: 36, AR050: 36, AR089: 4, AR061: 1 L0731: 19, L0766: 16,</p> | | |

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| | | | | Lys-170 to Gly-179, Thr-183 to Trp-188, Arg-193 to Glu-206, Asp-222 to Val-228, Ser-262 to Ser-277. | H0521: 11, L0748: 7, L0754: 7, L0806: 6, L0749: 6, L0794: 5, L0666: 5, S0360: 4, L0663: 4, L0740: 4, L0747: 4, H0656: 3, L0771: 3, L0662: 3, L0774: 3, L0665: 3, L0439: 3, L0777: 3, L0755: 3, H0638: 2, H0431: 2, H0620: 2, H0494: 2, S0002: 2, L0769: 2, L0803: 2, L0438: 2, H0689: 2, H0659: 2, H0658: 2, H0518: 2, S0206: 2, L0750: 2, S0242: 2, H0423: 2, H0650: 1, H0341: 1, H0661: 1, H0662: 1, H0300: 1, S0418: 1, S0376: 1, H0580: 1, S0045: 1, L0717: 1, H0453: 1, H0370: 1, H0497: 1, H0574: 1, H0632: 1, H0486: 1, L0021: 1, | | |
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| 10 | HDPSU48 | 1228284 | 20 | 466 - 987 | 633 | Gln-1 to Gly-8, Ile-15 to Asp-20; Lys-61 to Glu-69, Pro-93 to Lys-102, Ala-147 to Leu-156. | AR089: 1, AR061: 0 L0766: 10, L0803: 6, L0754: 5, S0152: 4, L0771: 3, H0656: 2, L0662: 2, L0774: 2. | S0474: 1, H0544: 1, H0046: 1, H0050: 1, H0510: 1, H0594: 1, S0340: 1, S0003: 1, T0023: 1, H0553: 1, H0644: 1, H0674: 1, H0040: 1, H0102: 1, H0641: 1, H0538: 1, L0763: 1, L0648: 1, L0768: 1, L0387: 1, L0804: 1, L0775: 1, L0805: 1, L0655: 1, L0783: 1, L0788: 1, S0374: 1, H0691: 1, H0435: 1, H0670: 1, H0648: 1, H0522: 1, H0134: 1, S3014: 1, L0779: 1, L0597: 1, S0026: 1, H0542: 1, H0543: 1, H0506: 1 and H0352: 1. | | |
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| | | | | | | Pro-159 to Asp-174. | S0380: 2, H0423: 2, H0624: 1, H0685: 1, L0002: 1, H0583: 1, L0760: 1, H0661: 1, S0358: 1, S0360: 1, H0637: 1, H0601: 1, H0486: 1, H0457: 1, H0247: 1, S0003: 1, T0067: 1, S0002: 1, S0426: 1, H0529: 1, L0770: 1, L0764: 1, L0806: 1, L0655: 1, L0659: 1, L0666: 1, L0663: 1, L0664: 1, S0428: 1, S0126: 1, H0435: 1, H0521: 1, H0522: 1, L0747: 1, L0756: 1, L0759: 1, H0445: 1 and H0422: 1. | | | |
| | | | | | | Ser-9 to Arg-14, Arg-48 to Arg-54, Gln-71 to Lys-77, Ile-91 to Asp-96, Lys-137 to Glu-145, Pro-169 to Lys-178, Ala-223 to Leu-232, | 909949 | 450 | 227 - 976 | 1063 |

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|----|---------|---------|----|----------|-----|---|--|--|--|--|
| 11 | HDPWE80 | 909916 | 21 | 94 - 765 | 634 | Pro-235 to Asp-250. Asp-8 to Cys-21, Val-25 to Asn-33, Thr-47 to Pro-55, Ala-62 to Thr-68, Val-79 to Lys-88, Asn-91 to Asn-104, Tyr-114 to Gly-120, Thr-187 to Glu-192, Ile-217 to Thr-224. | H0521: 9, L0595: 2, L0593: 1 and L0594: 1. | | | |
| 12 | HDQFY84 | 1092137 | 22 | 2 - 2776 | 635 | Glu-94 to Tyr-102, Pro-105 to Asn-112, Thr-121 to Gly-137, Glu-157 to Gly-162, Glu-179 to Phe-186, Cys-211 to Thr-222, Ser-240 to Lys-245, Thr-262 to Asn-279, Arg-288 to Pro-306, Asn-332 to Gln-339, Ser-375 to Leu-382, Arg-408 to Gly-415, Asp-423 to Thr-428, Ser-471 to Asn-476, Pro-545 to Gly-551, Ser-606 to Pro-616. | AR051: 2, AR050: 1, AR061: 1, AR054: 1, AR089: 0 S0354: 8, H0254: 2, S0358: 2, H0580: 2, H0521: 2, H0656: 1, H0590: 1, H0457: 1, H0271: 1 and H0488: 1. | | | |

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| H0333: 2, H0012: 2, T0010: 2, H0252: 2, H0063: 2, H0059: 2, S0002: 2, L0775: 2, L0655: 2, L0663: 2, L0665: 2, H0593: 2, H0658: 2, H0539: 2, H0555: 2, L0743: 2, L0744: 2, L0752: 2, L0731: 2, H0543: 2, H0624: 1, H0265: 1, H0650: 1, H0656: 1, S0212: 1, H0306: 1, H0305: 1, S0360: 1, S0046: 1, H0619: 1, S0222: 1, S6014: 1, H0613: 1, H0492: 1, H0250: 1, H0635: 1, H0427: 1, L0021: 1, H0036: 1, H0421: 1, H0399: 1, H0416: 1, H0188: 1, S0250: 1, L0143: 1, H0617: 1, H0673: 1, H0124: 1, H0163: 1, H0634: 1, H0087: 1, T0067: 1, | | | | | | |
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|----|---------|---------|-----|------------|------|---|--------------------------------------|--|--|--|
| 17 | HHFJF24 | 1212624 | 27 | 1374 - 538 | 640 | 1. | Lys-1 to Ala-6, Ser-38 to Gln-43. | AR089: 1, AR061: 0 S0001: 1, H0619: 1, H0586: 1, H0427: 1 and L0595: 1. | | |
| 18 | HHFMM10 | 910065 | 454 | 3 - 206 | 1067 | | | | | |
| | | 1178801 | 28 | 368 - 751 | 641 | Ser-19 to Thr-29, Lys-62 to Arg-67, Gln-102 to Phe-113. | | AR089: 20, AR061: 7 H0031: 2, H0619: 1 and S0036: 1. | | |
| | | 962997 | 455 | 95 - 493 | 1068 | Gly-1 to Ser-13, Ile-24 to Phe-29. | | | | |
| 19 | HHPBA42 | 901921 | 29 | 1 - 912 | 642 | Gly-9 to Gln-15. | | AR061: 133, AR089: 118 L0764: 4, L0659: 4, L0761: 3, S0360: 2, H0031: 2, L0662: 2, L0747: 2, L0750: 2, H0624: 1, H0295: 1, S0356: 1, S0132: 1, H0351: 1, L0394: 1, L0738: 1, H0051: 1, H0328: 1, L0796: 1, L0646: 1, L0800: 1, L0794: 1, L0549: 1, L0803: 1, L0806: 1, L0809: 1, L0788: 1, | | |

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|----|---------|---------|-----|---------|------|---|--|--|---|--|--|--|
| | | | | | | | | | L0789: 1, S0374: 1, H0435: 1, H0539: 1, S0378: 1, S0146: 1, L0754: 1, L0780: 1, L0752: 1 and L0591: 1. | | | |
| 20 | HHPSP89 | 1217052 | 30 | 2 - 916 | 643 | Gly-1 to Ile-11, Pro-49 to Asp-59, Val-64 to Leu-70, Gly-105 to Ser-112, Ser-130 to Ala-146, Asn-223 to Val-229, Asn-272 to Asp-278, Lys-294 to Tyr-305. | | | AR089: 1, AR061: 0 H0038: 3, H0616: 3, S0386: 2, L0366: 2, S0001: 1, S0360: 1, H0208: 1, S0046: 1, S6026: 1, H0486: 1, H0052: 1, H0201: 1, T0010: 1, S0036: 1, L0776: 1, S0216: 1, H0701: 1, H0593: 1, S0152: 1, H0521: 1, L0753: 1, L0758: 1 and S0031: 1. | | | |
| | | 910024 | 456 | 1 - 906 | 1069 | Pro-46 to Asp-56, Val-61 to Leu-67, Gly-102 to Ser-109, Ser-127 to Ala-143, Asn-220 to Val-226. | | | | | | |
| 21 | HKABX13 | 1167182 | 31 | 1 - 786 | 644 | Lys-49 to Trp-55, Tyr-66 to Val-79, Arg-89 to Asp-106, | | | AR089: 12, AR061: 2 H0556: 1, H0250: 1, H0494: 1, L0809: 1 and | | | |

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| | | | | | Gln-137 to Asn-142. | L0596: 1. | | |
| | 958656 | 457 | 2 - 763 | 1070 | Pro-I to Arg-15, Lys-49 to Trp-55, Tyr-66 to Val-79, Arg-89 to Asp-106, Gln-137 to Asn-142, Ala-171 to Tyr-178, Glu-224 to Ser-231. | | | |
| 22 | HLTHG77 | 1162409 | 32 | 2 - 406 | 645 | Met-17 to Met-24, Ser-31 to Asp-37, Leu-70 to Asp-97. | AR089: 0, AR061: 0 S0192: 13, L0471: 4, H0051: 4, H0413: 4, L0779: 4, S0418: 3, S0388: 3, H0591: 3, L0666: 3, S0242: 3, S0414: 2, H0012: 2, H0040: 2, H0100: 2, S0422: 2, L0766: 2, L0663: 2, S0152: 2, L0748: 2, L0439: 2, L0591: 2, S0196: 2, H0170: 1, H0686: 1, S0134: 1, S0282: 1, S0356: 1, S0045: 1, S0222: 1, H0441: 1, H0587: 1, T0039: 1, H0263: 1 T0110: 1 | |

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| | | | | | | H0050: 1, H0620: 1, H0266: 1, H0644: 1, L0055: 1, H0412: 1, H0494: 1, L0646: 1, L0662: 1, L0626: 1, L0768: 1, L0794: 1, L0375: 1, L0656: 1, H0547: 1, H0519: 1, H0672: 1, S0328: 1, H0134: 1, L0758: 1, S0031: 1, S0260: 1, L0608: 1, H0667: 1 and S0412: 1. | | |
| 23 | HLWBZ09 | 1179714 | 33 | 123 - 1349 | 646 | Met-14 to Met-21, Ser-28 to Asp-34, Leu-67 to Asp-94, Ala-109 to Ile-123. Val-9 to Arg-14, Glu-22 to Phe-30, Met-48 to Ser-59, Thr-76 to Lys-81, Ala-99 to Asp-104, Lys-122 to Val-144, Pro-159 to Glu-164, Gly-169 to His-183, Thr-188 to Asp-194, | AR089: 5, AR061: 3 L0748: 6, L0754: 4, L0775: 3, S0206: 3, L0758: 3, H0543: 3, H0309: 2, H0553: 2, H0644: 2, L0779: 2, L0752: 2, L0485: 2, L0600: 2, H0638: 1, S0356: 1, H0580: 1, | |

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| | | | | | | Lys-211 to Phe-218, Ser-230 to Pro-236, Ala-276 to Glu-281, Arg-297 to His-316, Ser-330 to Ser-335, Ser-367 to Thr-376, Pro-383 to Cys-394. | S0046: 1, L0717: 1, S0222: 1, H0635: 1, H0575: 1, S0010: 1, S6028: 1, S0316: 1, L0483: 1, H0032: 1, S0036: 1, H0038: 1, H0040: 1, H0623: 1, T0041: 1, H0494: 1, L0763: 1, L0774: 1, L0805: 1, L0776: 1, L0663: 1, H0519: 1, S0044: 1, H0436: 1, S0032: 1, L0744: 1, L0740: 1, L0747: 1, L0750: 1, L0757: 1, L0604: 1 and S0276: 1. | | |
| | | | | | | Val-9 to Arg-14, Glu-22 to Phe-30. | | | |
| 24 | HLWEH54 | 957912 | 459 | 112 - 477 | 1072 | Asn-38 to Tyr-46, Pro-56 to Asp-71, Asn-84 to Cys-96, Ser-110 to Val-142, Arg-181 to Leu-187, His-193 to Gly-198, Thr-201 to Arg-210, Asn-224 to Leu-230, | AR061: 0, AR089: 0, S0414: 12, L0740: 12, L0803: 9, L0438: 8, L0439: 6, L0756: 6, L0591: 6, H0623: 5, L0595: 5, L0769: 4, S0045: 3, S0046: 3, H0031: 3, L0771: 3, | | |

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| Thr-246 to Gly-251, Ser-267 to Ser-272, Ser-284 to Gln-290, Asp-294 to Asn-301, Asp-318 to Asn-324, Asn-338 to Glu-343, Gln-353 to Glu-362, Lys-374 to Lys-381, Asn-397 to Ala-409, Pro-426 to Tyr-436, Thr-469 to Pro-474, Ile-486 to Asn-492, Ile-499 to Ile-505, Lys-531 to Gln-539, Lys-585 to His-592, Lys-627 to Gly-635. | H0648: 3, L0747: 3, L0749: 3, H0341: 2, S0420: 2, S0356: 2, S0354: 2, S0222: 2, H0013: 2, H0575: 2, L0738: 2, H0046: 2, S0051: 2, S0003: 2, H0551: 2, H0413: 2, H0056: 2, H0529: 2, L0768: 2, L0794: 2, L0666: 2, H0547: 2, L0750: 2, L0779: 2, L0758: 2, L0686: 2, L0593: 2, S0412: 2, H0170: 1, L0441: 1, H0685: 1, H0381: 1, H0305: 1, S0007: 1, H0619: 1, S6026: 1, H0549: 1, H0550: 1, S6014: 1, H0586: 1, H0333: 1, H0559: 1, T0039: 1, H0156: 1, H0098: 1, H0036: 1, H0505: 1, H0327: 1, S0050: 1, H0051: 1, S0388: 1, T0010: 1, |
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| 27 | HMCFB47 | | | | | | Asp-96 to Pro-102, Pro-117 to Gly-124, Pro-132 to Ser-143. | | | | |
| | | 1151498 | 37 | 808 - 275 | 650 | | Arg-23 to Thr-29, Gly-45 to Arg-51, Pro-56 to Glu-66. | | | AR089: 31, AR061: 30 H0341: 1, H0050: 1, S0344: 1, L0750: 1 and L0366: 1. | |
| | | 910088 | 463 | 1 - 393 | 1076 | | Arg-8 to Pro-15, Gly-37 to Arg-46, Lys-59 to Leu-67, Ala-108 to Asp-113. | | | | |
| 28 | HMSOI20 | 1178817 | 38 | 417 - 2222 | 651 | | Arg-10 to His-17, Gln-24 to Asn-29, Glu-42 to His-51, Glu-63 to Asp-70, His-78 to Arg-84, Lys-101 to Phe-106, Phe-171 to Ser-180, Lys-182 to Gln-189, Pro-191 to Thr-197, Glu-236 to Ala-241, Gly-250 to Asn-256, Ser-293 to Ser-301, Lys-320 to Leu-325, Glu-334 to Val-340, Asp-453 to Gly-466, | | | AR061: 1, AR089: 0 L0748: 2, S0001: 1, H0575: 1, S0038: 1, S0426: 1, H0521: 1 and L0751: 1. | |

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| | | | | | | Pro-473 to Asp-478, Leu-576 to Lys-585. | | | | | | |
| | 928168 | 464 | 1 - 465 | 1077 | | Tyr-114 to Trp-119, Gln-124 to Ile-129. | | | | | | |
| 29 | HOENH55 | 1163460 | 39 | 1 - 624 | 652 | Asp-1 to Arg-7, Glu-19 to Leu-32, Leu-36 to Ser-49, Ser-74 to Pro-100, Ser-113 to Val-130, Thr-143 to His-154, Gln-161 to Arg-167, Val-194 to Phe-200. | | | | | AR061: 0, AR089: 0 S0126: 2, S0046: 1, H0645: 1, H0550: 1 and H0135: 1. | |
| | 922141 | 465 | 1 - 624 | 1078 | | Asp-1 to Arg-7, Glu-19 to Leu-32, Leu-36 to Ser-49, Ser-74 to Pro-100, Ser-113 to Val-130, Thr-143 to His-154, Gln-161 to Arg-167, Val-194 to Phe-200. | | | | | | |
| 30 | HPIA101 | 1078178 | 40 | 794 - 321 | 653 | Cys-52 to Trp-57, Pro-69 to Asp-74, Glu-95 to Ser-115, Pro-136 to Gly-143. | | | | | AR050: 204, AR054: 168, AR051: 151, AR089: 9, AR061: 6 S0140: 2, L0783: 2, S0150: 1, L0769: 1, L0774: 1, L0775: 1, | |

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|----|---------|---------|-----|-----------|------|--|--|--|--|
| 31 | HPJCT50 | 909928 | 466 | 288 - 764 | 1079 | Glu-48 to Leu-53. | L0809: 1, H0648: 1 and L0748: 1. | | |
| | | 1201773 | 41 | 32 - 1567 | 654 | Ser-3 to Trp-9, Arg-12 to Ser-18, Asp-42 to Gln-53, Arg-79 to Gly-90, Val-103 to Asp-108, Gly-175 to Asn-193, Ser-210 to Thr-217, Lys-242 to Glu-251, Glu-267 to Lys-273, Leu-287 to Lys-293, Ser-311 to Glu-318, Pro-335 to Lys-364, Asn-370 to Glu-376, Ala-392 to Thr-401. | AR089: 6, AR061: 4 H0561: 2, S0002: 2, H0521: 2, H0522: 2, H0656: 1, H0341: 1, H0550: 1, T0040: 1, H0036: 1, H0031: 1, H0560: 1, S0152: 1 and H0134: 1. | | |
| | | 919836 | 467 | 32 - 1567 | 1080 | Ser-3 to Trp-9, Arg-12 to Ser-18, Asp-42 to Gln-53, Arg-79 to Gly-90, Val-103 to Asp-108, Gly-175 to Asn-193, Ser-210 to Thr-217, Lys-242 to Glu-251, Glu-267 to Lys-273, | | | |
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| 32 | HPMFE91 | 1164740 | 42 | 605 - 1813 | 655 | Leu-287 to Lys-293, Ser-311 to Glu-318, Pro-335 to Lys-364, Asn-370 to Glu-376, Ala-392 to Thr-401. Glu-6 to Asp-20, Thr-25 to Lys-31, Lys-73 to Ala-95, Glu-102 to Phe-109, Pro-112 to Pro-118, Asp-136 to Leu-152, Val-246 to Thr-253, Thr-298 to Glu-303, Val-312 to Arg-322, Pro-341 to Arg-349, Lys-378 to Phe-388, Val-392 to Ala-397. | AR061: 3, AR089: 2 L0766: 10, L0752: 8, L0439: 6, L0747: 6, L0740: 5, L0756: 5, L0779: 4, L0777: 4, L0731: 4, S0051: 3, L0803: 3, L0774: 3, L0754: 3, S0360: 2, H0574: 2, L0763: 2, L0805: 2, L0809: 2, L0663: 2, L0751: 2, L0755: 2, L0759: 2, L0601: 2, H0624: 1, S0040: 1, S0298: 1, S0420: 1, H0580: 1, H0351: 1, H0600: 1, H0331: 1, H0013: 1, L0021: 1, H0575: 1, H0590: 1, T0110: 1, H0012: 1, H0615: 1, H0031: 1, H0553: 1, | | |
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| 35 | HSYCY88 | 914775 | 45 | 448 - 1089 | 658 | Leu-48 to Ser-55, Ser-63 to Ser-71, Asn-76 to Ala-82, Ser-87 to Phe-99, His-125 to Gly-140, Pro-160 to Asp-165. | AR089: 2, AR061: 2 L0751: 11, L0747: 7, H0009: 5, L0659: 5, L0731: 5, S0046: 4, L0663: 4, H0392: 3, H0024: 3, H0124: 3, H0135: 3, L0500: 3, L0662: 3, L0508: 3, L0493: 3, L0779: 3, L0777: 3, L0758: 3, L0759: 3, S0360: 2, S0007: 2, H0208: 2, H0486: 2, H0012: 2, H0620: 2, H0264: 2, L0770: 2, L0769: 2, L0648: 2, L0775: 2, L0438: 2, L0744: 2, L0439: 2, L0749: 2, L0756: 2, S0260: 2, H0171: 1, S0040: 1, | | |
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| | | | | S0420: 1, S0354: 1, S0045: 1, H0619: 1, H0549: 1, H0550: 1, H0592: 1, H0643: 1, H0427: 1, H0002: 1, H0599: 1, H0042: 1, H0575: 1, H0036: 1, H0590: 1, H0004: 1, H0618: 1, S0049: 1, H0597: 1, H0327: 1, H0150: 1, H0041: 1, L0471: 1, H0014: 1, H0051: 1, S6028: 1, S0250: 1, H0428: 1, H0622: 1, H0553: 1, H0644: 1, S0364: 1, H0551: 1, H0100: 1, S0112: 1, L0520: 1, L0502: 1, L0796: 1, L0771: 1, L0768: 1, L0497: 1, L0774: 1, L0378: 1, L0509: 1, L0776: 1, L0527: 1, L0515: 1, L0658: 1, L0809: 1, L0647: 1, L0790: 1, L0791: 1, | | | | |
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| 36 | HTEDW26 | 909749 | 46 | 3 - 959 | 659 | | | L0792: 1, L0666: 1, L0664: 1, L0665: 1, H0520: 1, H0547: 1, H0519: 1, S0126: 1, H0690: 1, H0658: 1, H0672: 1, H0651: 1, S0378: 1, S0380: 1, H0521: 1, S0037: 1, S0028: 1, L0743: 1, L0740: 1, L0750: 1 and L0757: 1. | | |
| | | | | | | | | AR061: 9, AR089: 9 H0521: 2, L0758: 2, H0038: 1, L0644: 1, L0645: 1, L0764: 1, L0662: 1, L0794: 1, L0557: 1, L0747: 1 and L0779: 1. | | |
| 37 | HTEKD92 | 1090524 | 47 | 263 - 1165 | 660 | Asn-11 to Pro-18, Tyr-31 to Asp-36, Asp-98 to Ser-119, Asp-142 to Glu-155, Gly-215 to Ile-226, Ser-237 to Ser-251, Leu-255 to Arg-260, His-263 to Asn-270, | | AR089: 1, AR061: 1 L0805: 11, L0779: 7, L0803: 5, L0789: 5, L0776: 4, L0794: 3, L0777: 3, H0575: 2, H0687: 2, S0003: 2, S0214: 2, L0766: 2, L0747: 2, L0731: 2, | | |

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| | | | | | Lys-287 to Thr-295. | H0662: 1, S0354: 1, H0549: 1, S0665: 1, T0048: 1, L0157: 1, H0031: 1, H0038: 1, S0002: 1, L0761: 1, L0800: 1, L0806: 1, L0787: 1, H0660: 1, S0330: 1, L0602: 1, S0206: 1, L0745: 1, L0756: 1, L0752: 1, L0759: 1, L0591: 1 and H0543: 1. | | |
| 38 | HTLDT05 | I227I27 | 48 | 625 - 2685 | 661 | Asn-11 to Pro-18, Tyr-31 to Asp-36, Asp-98 to Ser-119, Asp-142 to Glu-155, Gly-215 to Ile-226, Ser-237 to Ser-251, Leu-255 to Arg-260, His-263 to Asn-270, Lys-287 to Thr-295. Trp-3 to Thr-14, Ala-21 to Arg-30, Glu-66 to Pro-74, Pro-103 to Gly-108, Ile-135 to Ile-142 | AR089: 11, AR061: 7 H0253: 2, L0439: 1 and L0599: 1. | |

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| | | 529764 | 473 | 66 - 461 | 1086 | Gly-9 to Thr-14, Lys-37 to Arg-42, Asp-47 to Ser-54, Asp-58 to Lys-63, Lys-82 to Asn-89. | | | | | |
| 40 | HTPHM71 | 1194698 | 50 | 1 - 1836 | 663 | Tyr-17 to Val-23, Ala-54 to Leu-65, Arg-115 to Asn-120, Ser-150 to Ser-158, Glu-234 to Ile-251, His-272 to Asn-277, Gly-284 to Gln-303, Glu-327 to Lys-332, Thr-362 to Leu-368, Leu-390 to Asn-399, Ser-432 to Tyr-444, Asn-456 to Thr-467, Ser-474 to Thr-484, Asn-505 to Leu-510, Gln-563 to Ser-568, Ala-575 to Cys-582. | | | | AR061: 4, AR089: 2 L0748: 8, H0040: 5, H0039: 3, L0766: 3, H0663: 2, T0040: 2, L0659: 2, L0754: 2, L0756: 2, H0556: 1, H0583: 1, H0650: 1, H0013: 1, H0318: 1, H0194: 1, H0596: 1, H0545: 1, S0003: 1, H0622: 1, H0634: 1, H0641: 1, H0647: 1, L0643: 1, L0794: 1, L0803: 1, S0052: 1, H0520: 1, H0539: 1, H0555: 1 and L0595: 1. | |
| | | 909878 | 474 | 3 - 1094 | 1087 | Tyr-14 to Phe-24. | | | | | |

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|----|---------|---------|-----|------------|------|----|--|---|--|--|
| 41 | HUUAR12 | 1194702 | 51 | 1 - 975 | 664 | 4. | Pro-1 to Gln-11, Leu-36 to Gln-42, Glu-81 to Trp-86, Arg-108 to Lys-113, Arg-143 to Asn-149, Glu-154 to Asp-160, Glu-169 to His-174, Trp-184 to Ser-189, Lys-210 to Trp-217, Lys-233 to Tyr-239, Asp-308 to Gly-315. | AR089: 1, AR061: 1 L0809: 9, L0775: 3, L0758: 3, S0376: 2, L0439: 2, L0752: 2, H0656: 1, H0661: 1, H0586: 1, H0590: 1, H0594: 1, L0769: 1, L0761: 1, L0800: 1, L0662: 1, L0766: 1, L0803: 1, L0651: 1, L0805: 1, L0659: 1, L0788: 1, L0666: 1, L0779: 1 and S0276: 1. | | |
| | | 944393 | 475 | 3 - 716 | 1088 | | | | | |
| 42 | HWAGP22 | 1150195 | 52 | 310 - 1713 | 665 | | Gly-8 to Gly-15, Ser-25 to Ser-30, Glu-65 to Ala-71. | AR089: 1, AR061: 1 L0751: 7, H0575: 2, H0617: 2, H0634: 2, L0438: 2, L0747: 2, L0601: 2, H0556: 1, S0040: 1, H0484: 1, H0306: 1, S0360: 1, H0550: 1, H0607: 1, H0586: 1, H0004: 1, H0581: 1, H0288: 1, H0553: 1, H0100: 1, | | |

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| | | | | | | | | | T0042: 1, L0764: 1, L0766: 1, L0653: 1, S0052: 1, H0144: 1, H0701: 1, L0777: 1, S0192: 1, H0542: 1 and H0543: 1. | | |
| | 909919 | 476 | 3 - 1151 | 1089 | Arg-15 to Leu-23, Glu-70 to Lys-76, Lys-96 to Gln-102, Leu-119 to Arg-124, Ala-141 to Glu-146, Leu-159 to Glu-169, Thr-195 to Lys-202, Gln-239 to Gly-251. | | | | | | |
| 43 | HWBCE37 | 906968 | 53 | 3 - 431 | 666 | | | | AR089: 1, AR061: 0 H0580: 1 and H0427: 1. | | |
| 44 | HWLFB60 | 1223499 | 54 | 2 - 2233 | 667 | Gly-1 to Lys-8, Arg-52 to Gly-57, Asp-69 to Ser-74, Arg-90 to Lys-97, Asp-126 to Thr-132, Cys-155 to Thr-171, Lys-189 to Ala-198, Lys-239 to Ser-245, Gln-260 to Ser-276, | | | AR089: 6, AR061: 0 L0766: 4, L0666: 4, L0439: 4, S0354: 3, H0014: 3, H0551: 3, H0529: 3, L0665: 3, H0519: 3, L0740: 3, L0759: 3, H0656: 2, S0003: 2, H0553: 2, L0775: 2, L0657: 2, | | |

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| Ser-295 to Glu-302, Asp-307 to Leu-319, Ser-332 to Leu-347, Ser-363 to Ala-371, Ser-429 to Asp-436, Ala-458 to Asn-463, Pro-477 to Asn-483, Ile-587 to Tyr-594, Lys-603 to His-611, Pro-620 to Ser-625, Lys-661 to Trp-677, Glu-700 to Glu-714. | H0144: 2, H0435: 2, H0521: 2, L0747: 2, S0260: 2, L0593: 2, H0423: 2, S0424: 2, H0171: 1, H0556: 1, S0114: 1, S0430: 1, S0212: 1, S0400: 1, H0662: 1, S0356: 1, S0358: 1, S0045: 1, S0046: 1, S0132: 1, H0351: 1, H0411: 1, H0431: 1, H0587: 1, H0486: 1, H0036: 1, S0010: 1, H0318: 1, H0052: 1, H0085: 1, H0596: 1, H0046: 1, T0010: 1, S6028: 1, S0312: 1, L0055: 1, H0038: 1, H0040: 1, H0264: 1, H0494: 1, S0294: 1, H0509: 1, H0641: 1, H0647: 1, S0144: 1, S0208: 1, L0637: 1, L0761: 1, L0646: 1, L0765: 1, L0771: 1, L0768: 1. |
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| 47 | HE6BK63 | | | | | | | | L0752: 2, L0755: 2, H0590: 1, H0014: 1, S0250: 1, L0772: 1, L0764: 1, L0804: 1, H0522: 1, S0406: 1, L0754: 1, L0779: 1, L0731: 1 and L0758: 1. | | |
| | | 949702 | 479 | 551 - 339 | 1092 | Lys-1 to Thr-7, Arg-34 to Pro-41. | | | | | |
| | | 1153879 | 57 | 3 - 767 | 670 | Gly-2 to Asp-11, Ser-71 to Gln-78, Ser-110 to Asn-117, Ser-155 to Ser-162, Thr-171 to Asp-181, Arg-193 to Leu-203, Arg-207 to Thr-215, Ala-225 to Lys-246, Lys-248 to Leu-255. | | | AR054: 21, AR050: 18, AR089: 17, AR051: 17, AR061: 14 H0090: 2, H0100: 2, L0792: 2, H0052: 1, H0012: 1, H0212: 1, S0426: 1, L0800: 1, L0663: 1, L0743: 1, L0756: 1 and L0780: 1. | | |
| | | 661045 | 480 | 586 - 1191 | 1093 | Ser-12 to Gln-19, Ser-51 to Asn-58, Ser-96 to Ser-103, Thr-112 to Asp-122, Arg-134 to Leu-144, Arg-148 to Thr-156, Ala-166 to Lys-187, Lys-189 to Gly-200. | | | | | |

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| 50 | HAAAO58 | 909835 | 482 | 634 - 1146 | 1095 | Pro-107 to Arg-120. Arg-11 to Pro-17, Glu-43 to Gln-50, Gln-74 to Gln-85, Leu-127 to Asn-132, Arg-141 to Lys-146. | AR089: 43, AR061: 8 H0592: 2, H0009: 1, H0030: 1, L0143: 1, H0264: 1, H0646: 1, L0653: 1, L0665: 1, S0052: 1 and H0658: 1. | | |
| | | 1091088 | 60 | 15 - 467 | 673 | | | | |
| | | 912622 | 483 | 15 - 467 | 1096 | Arg-11 to Pro-17, Glu-43 to Gln-50, | | | |
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H0633: 1, S0144: 1,
S0426: 1, L0639: 1,
L0637: 1, L0761: 1,
L0646: 1, L0644: 1,
L0764: 1, L0766: 1,
L0803: 1, L0775: 1,
L0375: 1, L0652: 1,
L0655: 1, L0384: 1,
L0382: 1, L0663: 1,
L0664: 1, L0665: 1,
S0052: 1, H0144: 1,
H0547: 1, L0741: 1,
L0743: 1, L0740: 1,
L0750: 1, H0595: 1,
L0588: 1, L0601: 1,
S0276: 1, H0423: 1,
H0422: 1 and H0352: 1.

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| 51 | HADFK69 | 1091937 | 61 | 201 - 782 | 674 | Gln-74 to Gln-85. Glu-1 to Gly-6, Glu-50 to Val-55, Tyr-62 to Leu-67, Glu-105 to Lys-113, Ser-127 to Val-132, Ala-141 to Val-146, Thr-154 to Leu-159, Leu-170 to Ser-177, Pro-182 to Asn-194. | AR089: 4, AR061: 1 L0794: 3, L0803: 3, L0809: 3, S0222: 2, L0747: 2, L0756: 2, L0752: 2, L0758: 2, H0171: 1, L0002: 1, S0420: 1, S6026: 1, H0427: 1, L0021: 1, H0051: 1, T0010: 1, H0032: 1, S0422: 1, L0775: 1, L0659: 1, L0367: 1, L0790: 1, L0666: 1, L0744: 1, L0754: 1, L0779: 1, L0777: 1 and L0757: 1. | | |
| 52 | HDPMO62 | 912850 1152329 | 484 62 | 1 - 573 1 - 447 | 1097 675 | Gly-38 to Pro-48, Pro-105 to Ser-116, Arg-120 to Ser-127, Ser-142 to Ser-149. Ala-14 to Gly-20, Gly-34 to Pro-44, His-128 to Ser-134. | AR089: 1 S0002: 2 and H0522: 1. | | |
| 53 | HDPMO85 | 912722 1228282 | 485 63 | 1 - 582 138 - 719 | 1098 676 | Glu-58 to Ala-72, Thr-91 to Gln-98. | AR089: 8, AR061: 2 L0759: 15, L0766: 9, | | |

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| | | | | | Glu-106 to Glu-115, Gln-128 to Asp-134, Lys-143 to Lys-148, Lys-170 to Ser-178, Ser-183 to Gly-190. | L0754: 8, L0769: 6, S0126: 6, L0439: 6, S0360: 5, L0776: 5, S0027: 5, L0731: 5, H0556: 4, H0341: 4, H0641: 4, L0747: 4, L0750: 4, L0596: 4, L0588: 4, H0650: 3, H0637: 3, H0013: 3, H0644: 3, H0412: 3, H0560: 3, L0809: 3, S0330: 3, H0521: 3, L0742: 3, H0543: 3, H0624: 2, H0171: 2, S0134: 2, H0656: 2, S0354: 2, S0007: 2, H0351: 2, H0333: 2, H0492: 2, H0599: 2, H0618: 2, H0581: 2, H0620: 2, S0051: 2, T0010: 2, H0594: 2, H0628: 2, H0090: 2, H0591: 2, H0264: 2, T0042: 2, L0641: 2, L0794: 2, L0774: 2, L0527: 2, L0659: 2, | |
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| | | | | | L0545: 2, L0666: 2, L0665: 2; H0520: 2, H0435: 2, H0522: 2, H0576: 2, S0028: 2, L0749: 2, L0756: 2, L0753: 2, L0601: 2, L0603: 2, H0265: 1, S0114: 1, S0116: 1, S0212: 1, H0402: 1, S0418: 1, S0420: 1, H0340: 1, H0489: 1, S0045: 1, S0222: 1, H0370: 1, H0486: 1, T0109: 1, H0427: 1, H0036: 1, S0010: 1, L0563: 1, H0263: 1, H0597: 1, H0545: 1, H0150: 1, H0009: 1, H0123: 1, H0050: 1, L0471: 1, H0024: 1, S0214: 1, H0604: 1, H0030: 1, H0031: 1, L0055: 1, H0124: 1, S0366: 1, H0551: 1, H0477: 1, H0487: 1, H0268: 1, H0623: 1, |
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| | | | | | | L0564: 1, H0022: 1, S0150: 1, H0633: 1, S0144: 1, L0770: 1, L0637: 1, L0761: 1, L0646: 1, L0764: 1, L0773: 1, L0662: 1, L0768: 1, L0381: 1, L0803: 1, L0775: 1, L0651: 1, L0653: 1, L0783: 1, L0789: 1, L0791: 1, L0792: 1, L0663: 1, S0428: 1, L0438: 1, H0547: 1, H0659: 1, H0658: 1, H0670: 1, H0672: 1, H0539: 1, H0518: 1, H0436: 1, S3014: 1, L0740: 1, L0751: 1, L0777: 1, L0780: 1, L0752: 1, L0755: 1, H0444: 1, H0445: 1, H0343: 1, L0592: 1, H0667: 1, H0136: 1, S0192: 1, S0194: 1, H0542: 1 and H0352: 1. | |
| 912837 | 486 | 138 - 719 | 1099 | Glu-5] to Val-56. | | | |

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| | L0756: 2, L0588: 2, L0591: 2, L0595: 2, S0011: 2, H0542: 2, L0697: 2, H0171: 1, H0265: 1, S6024: 1, S0114: 1, H0657: 1, H0656: 1, H0341: 1, S0282: 1, H0384: 1, H0255: 1, H0671: 1, H0661: 1, H0589: 1, L0005: 1, S0376: 1, S0360: 1, S0408: 1, H0152: 1, H0393: 1, L0717: 1, H0437: 1, H0462: 1, H0549: 1, S6016: 1, S0220: 1, H0431: 1, H0392: 1, H0298: 1, H0587: 1, H0333: 1, H0331: 1, H0632: 1, S0414: 1, T0039: 1, H0635: 1, H0036: 1, H0590: 1, S0346: 1, S0049: 1, H0544: 1, H0041: 1, H0050: 1, H0014: 1, H0355: 1, H0510: 1, | |
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| | H0375: 1, H0594: 1, H0687: 1, H0553: 1, H0644: 1, L0055: 1, H0383: 1, H0169: 1, H0064: 1, H0708: 1, H0068: 1, H0598: 1, H0135: 1, H0038: 1, H0616: 1, H0413: 1, H0056: 1, S0112: 1, L0564: 1, H0280: 1, H0494: 1, H0625: 1, H0561: 1, S0344: 1, H0538: 1, L0763: 1, L0761: 1, L0772: 1, L0646: 1, L0800: 1, L0773: 1, L0662: 1, L0794: 1, L0650: 1, L0651: 1, L0806: 1, L0654: 1, L0528: 1, L0663: 1, H0144: 1, S0374: 1, H0520: 1, H0682: 1, H0659: 1, H0660: 1, H0648: 1, S0328: 1, S0330: 1, H0539: 1, S0380: 1, H0518: 1, S0146: 1, | | | | | | |
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| 56 | HE8TB94 | 1178794 | 66 | 470 - 1087 | 679 | Ser-95 to Gly-103, Thr-114 to Asn-120. | AR089: 2, AR061: 1 L0747: 10, H0266: 6, H0623: 6, L0740: 5, S0045: 3, H0050: 3, H0551: 3, L0777: 3, L0757: 3, L0759: 3, L0588: 3, H0056: 2, S0404: 2, L0745: 2, L0780: 2, L0589: 2, H0624: 1, H0170: 1, S0360: 1, H0329: 1, H0645: 1, H0437: 1, H0601: 1, H0486: 1, H0013: 1, H0123: 1, L0471: 1, H0328: 1, H0622: 1, H0591: 1, H0433: 1, H0413: 1, H0100: 1, S0210: 1, L0769: 1, L0659: 1, L0788: 1, S0126: 1, S0044: 1, S0146: 1, H0555: 1, S0037: 1, S0027: 1, L0748: 1, L0439: 1 and L0465: 1. | | |
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| 57 | HE8UB55 | 935935 | 489 | 430 - 1104 | 1102 | Cys-14 to Lys-31, Thr-87 to Leu-99, Arg-149 to Thr-154, Pro-208 to Ser-220. | AR061: 2, AR089: 2 L0766: 3, H0556: 2, H0662: 2, S0420: 2, H0013: 2, H0457: 2, H0622: 2, L0659: 2, H0520: 2, S0152: 2, S0136: 2, H0521: 2, L0731: 2, H0624: 1, S0376: 1, S0132: 1, H0619: 1, L0021: 1, H0581: 1, H0251: 1, H0105: 1, H0373: 1, S0003: 1, H0328: 1, H0615: 1, H0553: 1, H0644: 1, H0628: 1, S0036: 1, H0551: 1, H0264: 1, H0623: 1, H0494: 1, S0144: 1, H0529: 1, L0783: 1, H0144: 1, S0126: 1, H0435: 1, S0328: 1, S0330: 1, H0539: 1, | | |
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| 58 | HEBGA65 | 912932 | 1178633 | 68 | 309-977 | 681 | 1103 | Glu-37 to Thr-42. | Lys-35 to Val-45, Ser-133 to Ala-138, Asp-162 to Asp-174, Gln-179 to Cys-186, Arg-214 to Pro-223. | AR089: 1, AR061: 0 L0748: 5, H0559: 3, H0009: 3, H0318: 2, H0581: 2, H0052: 2, H0135: 2, H0494: 2, L0770: 2, L0766: 2, L0809: 2, L0789: 2, L0439: 2, L0751: 2, L0755: 2, L0758: 2, L0604: 2, H0352: 2, S0040: 1, H0583: 1, H0671: 1, H0661: 1, H0402: 1, S0360: 1, S0007: 1, H0645: 1, H0351: 1, H0392: 1, H0587: 1, S0005: 1, H0156: 1, L0021: 1, H0545: 1, H0012: 1, H0024: 1, L0183: 1, | | |
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| 59 | HEGBB59 | 1197907 | 69 | 398 - 1078 | 682 | Thr-158 to Gly-163, Gly-195 to Tyr-201. Tyr-1 to Asp-11, Asp-64 to His-73, Ala-90 to Gly-100, Ile-133 to Asn-138, Val-195 to His-213. | AR061: 2, AR089: 2 L0731: 5, L0439: 4, H0662: 2, H0369: 2, L0105: 2, H0622: 2, L0794: 2, L0803: 2, L0804: 2, L0775: 2, L0809: 2, H0547: 2, L0754: 2, L0758: 2, L0485: 2, H0484: 1, S0360: 1, H0550: 1, H0441: 1, H0392: 1, H0031: 1, H0644: 1, L0369: 1, L0662: 1, L0768: 1, L0790: 1, L0663: 1, L0664: 1, S0126: 1, H0555: 1, L0756: 1, L0589: 1, L0592: 1, L0599: 1 and H0506: 1. | | |
| | | 912601 | 492 | 265 - 645 | 1105 | Tyr-1 to Asp-11, Asp-64 to His-73, Ala-90 to Ile-96. | | | |
| 60 | HELHC48 | 956003 | 70 | 816 - 403 | 683 | Ile-3 to Thr-11, Asn-31 to Lys-40, | AR061: 2, AR089: 1 L0439: 22, L0770: 11, | | |

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| | L0664: 2, H0144: 2, H0520: 2, S0126: 2, H0690: 2, S0152: 2, L0748: 2, L0780: 2, L0758: 2, S0260: 2, L0604: 2, L0601: 2, H0542: 2, H0422: 2, S0424: 2, H0624: 1, H0170: 1, T0049: 1, S0134: 1, H0650: 1, H0661: 1, H0638: 1, S0418: 1, S0354: 1, H0637: 1, H0580: 1, S0132: 1, H0645: 1, H0393: 1, L0717: 1, H0437: 1, H0549: 1, H0441: 1, H0431: 1, H0497: 1, H0486: 1, T0039: 1, H0156: 1, T0082: 1, H0590: 1, S0010: 1, H0505: 1, H0596: 1, L0040: 1, H0544: 1, H0545: 1, L0157: 1, H0050: 1, L0471: 1, H0024: 1, H0375: 1, H0687: 1. | | | | | | |
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| | | | | | | | | L0756: 1, L0777: 1, L0599: 1, L0608: 1, L0366: 1, S0011: 1, H0653: 1, S0192: 1, S0194: 1, H0543: 1 and S0452: 1. | | |
| 61 | HQQH90 | 1212646 | 71 | 3 - 680 | 684 | Arg-14 to Cys-25, Ala-90 to Arg-96, Ile-115 to Asp-122, Lys-147 to Ser-152, Ala-202 to Gln-208, Asp-211 to Ser-221. | | AR089: 4, AR061: 2 H0457: 11, H0052: 3, H0580: 2, H0529: 2, L0655: 2, L0748: 2, L0439: 2, L0779: 2, H0261: 1, H0486: 1, L0021: 1, H0575: 1, T0071: 1, H0194: 1, L0579: 1, H0087: 1, H0264: 1, T0041: 1, H0695: 1, L0766: 1, L0803: 1, L0775: 1, L0758: 1 and H0422: 1. | | |
| | | 907532 | 493 | 1 - 666 | 1106 | Arg-10 to Cys-21. | | | | |
| 62 | HFKHA18 | 1152242 | 72 | 1 - 690 | 685 | Gly-7 to Pro-13, Cys-19 to Gly-25, Phe-51 to Lys-61, Ala-88 to Phe-93, Leu-130 to Ser-136, Ala-221 to Cys-228. | | AR089: 4, AR061: 4 H0666: 12, S0358: 10, H0620: 10, L0750: 8, L0747: 7, L0731: 7, H0135: 5, L0659: 5, L0740: 5, L0757: 5, | | |

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| S0360: 4, H0123: 4, S0022: 4, L0666: 4, L0665: 4, S0028: 4, L0748: 4, L0777: 4, L0588: 4, H0265: 3, S0420: 3, H0208: 3, H0046: 3, H0024: 3, H0284: 3, H0100: 3, L0650: 3, L0375: 3, L0382: 3, H0651: 3, L0755: 3, H0352: 3, S0278: 2, H0592: 2, H0333: 2, H0253: 2, H0544: 2, H0545: 2, H0081: 2, H0012: 2, H0266: 2, H0286: 2, H0252: 2, H0428: 2, H0628: 2, H0551: 2, S0210: 2, L0763: 2, L0770: 2, L0774: 2, L0518: 2, L0809: 2, H0547: 2, H0682: 2, H0670: 2, S0037: 2, S0027: 2, L0751: 2, L0752: 2, L0758: 2, L0601: 2, H0668: 2, | | | | | | |
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| S0194: 2, H0170: 1, H0556: 1, H0686: 1, S0040: 1, H0295: 1, H0341: 1, H0638: 1, S0418: 1, S0376: 1, S0444: 1, H0580: 1, H0329: 1, S0468: 1, S0045: 1, S0046: 1, S0132: 1, H0619: 1, H0645: 1, L0717: 1, H0549: 1, H0550: 1, H0586: 1, H0587: 1, L0021: 1, H0575: 1, H0581: 1, H0052: 1, H0309: 1, H0546: 1, H0457: 1, H0150: 1, H0041: 1, H0050: 1, L0163: 1, H0051: 1, H0615: 1, H0688: 1, H0031: 1, H0634: 1, H0087: 1, H0334: 1, H0633: 1, H0646: 1, L0772: 1, L0643: 1, L0764: 1, L0662: 1, L0767: 1, L0775: 1, L0651: 1, L0806: 1, | | | | | | |
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| 63 | HFKMA10 | 964258 | 73 | 2 - 766 | 686 | 1107 | Gly-5 to Pro-11, Cys-17 to Gly-23, Phe-49 to Lys-59, Ala-86 to Phe-91, Leu-128 to Ser-134, Asn-209 to Asn-214. | 972414 | 494 | 1 - 684 | 1107 | L0776: 1, L0656: 1, L0783: 1, L0383: 1, L0543: 1, L0789: 1, L0663: 1, H0593: 1, H0684: 1, H0659: 1, H0658: 1, H0660: 1, H0709: 1, S0152: 1, H0521: 1, H0627: 1, L0611: 1, L0439: 1, L0745: 1, L0759: 1, L0593: 1, L0361: 1, L0603: 1, S0026: 1, H0667: 1 and H0506: 1. | 17q25 | 114290, 138033, 162100, 170500, 170500, 170500, 180860, |
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| 64 | HHBFM91 | 1092116 | 74 | 3 - 506 | 687 | Ala-19 to Phe-24, Thr-45 to Val-53, Ile-77 to Arg-83, Ser-105 to Gly-111, Gln-128 to Ala-144, Asp-153 to Gly-161. | S0031: 1. AR089: 8, AR061: 1 H0575: 2, S0031: 2, S0134: 1, H0156: 1, H0373: 1, H0328: 1, H0135: 1, S0428: 1, H0682: 1, H0435: 1, H0518: 1, H0521: 1, L0779: 1 and L0758: 1. | | | 264470 |
| 65 | HIBBF63 | 912832 | 495 | 2 - 343 | 1108 | Thr-3 to Arg-10, Lys-71 to Lys-80, Glu-107 to Arg-120, Lys-128 to Gly-133. | L0748: 2, H0052: 1, H0194: 1, T0010: 1, H0658: 1, S0380: 1 and L0366: 1. | 16p13.3 | | 141750, 141800, 141800, 141800, 141800, 141850, 141850, 141850, 141850, 141850, 141850, 156850, 186580, 191092, 600140, 600273, 601313. |

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| 66 | HMCEI38 | 1134410 | 76 | 190 - 627 | 689 | Gln-21 to Ala-28, Tyr-55 to Phe-60, Tyr-78 to Ile-84. | AR061: 4, AR089: 2 H0645: 1, H0494: 1, S0142: 1, H0593: 1 and H0435: 1. | | 601785 |
| | | 912580 | 496 | 189 - 626 | 1109 | Gln-21 to Ala-28, Tyr-55 to Phe-60, Tyr-78 to Ile-84. | | | |
| | | 1154790 | 77 | 1181 - 3 | 690 | Pro-7 to Ile-20, Arg-26 to Trp-36, Trp-68 to Thr-88, Pro-96 to Gly-101, Ser-109 to Arg-117, Pro-163 to Ala-169, Asp-260 to Asp-266. | AR061: 6, AR089: 5 H0641: 4, H0521: 4, S0418: 2, H0617: 2, L0794: 2, H0436: 2, L0748: 2, L0596: 2, H0556: 1, S0134: 1, H0650: 1, H0657: 1, H0341: 1, S0001: 1, H0638: 1, S0358: 1, S0045: 1, S0278: 1, S0474: 1, H0545: 1, H0081: 1, H0271: 1, H0416: 1, H0551: 1, H0623: 1, H0059: 1, S0344: 1, L0761: 1, L0803: 1, L0804: 1, L0383: 1, H0435: 1, S0152: 1, H0522: 1, | | |
| 67 | HMWJD68 | | | | | | | | |

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| | | | | | | H0015: 1, H0107: 1, H0083: 1, H0510: 1, S6028: 1, H0252: 1, H0622: 1, H0272: 1, H0100: 1, H0494: 1, S0144: 1, L0800: 1, L0768: 1, L0794: 1, L0804: 1, L0806: 1, H0689: 1, H0672: 1, S0328: 1, H0631: 1, S0028: 1, L0749: 1, L0750: 1, L0780: 1, L0755: 1, L0759: 1, S0434: 1, L0592: 1, H0668: 1 and H0423: 1. | | |
| 70 | HSHAV32 | 1180388 | 80 | 157 - 627 | 693 | Asn-40 to Asn-47, Ala-74 to Gly-89, Thr-100 to Asn-106, Gly-129 to Glu-139, Ile-182 to Gly-193, Arg-204 to Ser-211. Phe-49 to Lys-55. | AR089: 4, AR061: 3 L0731: 7, L0749: 6, L0105: 5, H0046: 5, L0748: 5, H0551: 4, L0747: 4, L0777: 4, | |

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| | | | | | | | | S0040: 3, L0663: 3, S0152: 3, L0659: 2, H0547: 2, L0439: 2, L0779: 2, L0448: 1, H0685: 1, H0341: 1, H0663: 1, H0580: 1, L0021: 1, H0594: 1, S0214: 1, H0615: 1, H0628: 1, H0561: 1, H0646: 1, L0640: 1, L0662: 1, L0774: 1, L0783: 1, L0809: 1, L0666: 1, H0144: 1, L0352: 1, S3012: 1, S0037: 1, L0754: 1, L0756: 1, L0752: 1, L0755: 1, L0759: 1, H0667: 1 and S0192: 1. | | |
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| | | | | | S0132: 2, H0549: 2, H0587: 2, L0764: 2, L0773: 2, L0659: 2, L0382: 2, L0809: 2, L0519: 2, H0593: 2, L0752: 2, L0596: 2, L0595: 2, H0506: 2, H0294: 1, H0483: 1, H0661: 1, S0358: 1, S0444: 1, L0717: 1, H0370: 1, H0318: 1, H0234: 1, H0597: 1, H0024: 1, H0622: 1, H0553: 1, H0212: 1, H0135: 1, H0087: 1, H0059: 1, H0100: 1, H0538: 1, L0763: 1, L0772: 1, L0646: 1, L0645: 1, L0648: 1, L0364: 1, L0649: 1, L0774: 1, L0806: 1, L0776: 1, L0657: 1, L0540: 1, L0542: 1, L0383: 1, L0529: 1, L0664: 1, L0665: 1, H0682: 1, H0683: 1, | | |
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| 75 | HUVFX92 | 912929 | 503 | 3 - 320 | 1116 | Ile-12 to Asn-17, Val-74 to His-92. | Asp-47 to Ser-53, Ala-82 to Arg-88. | AR061: 0, AR089: 0 H0623: 2, S0045: 1 and H0620: 1. | | | |
| 76 | HWAE71 | 1182321 | 86 | 1 - 717 | 699 | Pro-17 to His-22. | | AR089: 6, AR061: 1 L0740: 2 and H0581: 1. | | | |
| | | 931547 | 505 | 2 - 553 | 1118 | Gln-60 to Ala-68, Trp-132 to Ser-138, Lys-156 to Val-163. | | | | | |

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| 77 | HWAHD49 | 1228064 | 87 | 151 - 1011 | 700 | 3. Arg-12 to Leu-19, Gly-56 to Pro-62, Cys-68 to Gly-74, Phe-100 to Lys-110, Ala-137 to Phe-142, Leu-179 to Ser-185, Ala-278 to Cys-285. | AR089: 9, AR061: 3 S0358: 10, L0747: 7, L0750: 7, L0731: 7, H0620: 5, L0659: 5, S0360: 4, S0022: 4, L0666: 4, L0665: 4, L0748: 4, L0740: 4, L0777: 4, L0757: 4, L0588: 4, H0265: 3, S0420: 3, H0046: 3, H0135: 3, H0100: 3, L0650: 3, L0375: 3, L0382: 3, H0651: 3, S0028: 3, L0755: 3, H0352: 3, S0278: 2, H0592: 2, H0333: 2, H0253: 2, H0544: 2, H0123: 2, H0081: 2, H0012: 2, H0252: 2, H0428: 2, L0763: 2, L0770: 2, L0774: 2, L0518: 2, L0809: 2, H0682: 2, S0037: 2, S0027: 2, L0751: 2, L0758: 2, H0170: 1, | | |
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| | | | | | | | | | Arg-12 to Leu-19, Gly-56 to Pro-62, Cys-68 to Gly-74, Phe-100 to Lys-110, Ala-137 to Phe-142, Leu-179 to Phe-185. | | |
| | | | | | | | | | Thr-1 to Gln-18, Thr-55 to His-60, Ala-91 to Gln-102, Ser-117 to His-124, Val-132 to Gly-139, Lys-148 to Gly-158, Glu-220 to Lys-234, Gln-253 to Gly-260, Asp-274 to Pro-281, Gln-318 to Val-326, | | |
| 78 | HWLGG31 | 1178825 | 88 | 3 - 1205 | 701 | | | | AR089: 2, AR061: 2 S0007: 4, L0747: 3, S0222: 2, H0599: 2, H0318: 2, L0764: 2, L0662: 2, S0354: 1, H0706: 1, S0010: 1, S0049: 1, H0052: 1, H0031: 1, H0040: 1, H0634: 1, H0100: 1, L0761: 1, L0772: 1, | | |

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| | | | | | | Pro-334 to Glu-344, Gln-382 to Pro-389. | L0646: 1, L0773: 1, L0803: 1, L0375: 1, L0651: 1, L0636: 1, L0664: 1, H0522: 1, L0439: 1, L0779: 1, L0777: 1, L0731: 1 and H0136: 1. | | |
| | 912581 | 507 | 2 - 565 | 1120 | | Arg-1 to Gln-15, Thr-52 to His-57, Ala-88 to Gln-99, Ser-114 to His-121, Val-129 to Gly-136. | | | |
| 79 | HWLKF25 | 1089052 | 89 | 224 - 886 | 702 | Val-49 to Gln-56, Ala-85 to Leu-93, Pro-96 to Ala-101, Val-110 to Asn-118, Asp-131 to Glu-136, Lys-146 to Ala-159, Met-164 to Tyr-169, Thr-174 to Thr-180. | AR061: 3, AR089: 2 S0358: 1, H0052: 1, L0803: 1 and L0759: 1. | | |
| | 912842 | 508 | 224 - 889 | 1121 | | Val-49 to Gln-56, Ala-85 to Leu-93, Pro-96 to Ala-101, Val-110 to Asn-118, Asp-131 to Glu-136, Lys-146 to Ala-159. | | | |

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| 80 | H2CBH45 | 963811 | 90 | 2 - 421 | 703 | Met-164 to Tyr-169, Thr-174 to Thr-180, Ser-213 to Gly-218. | AR061: 3, AR089: 3 H0437: 1, S0280: 1, T0110: 1, H0622: 1, L0745: 1, L0746: 1, L0731: 1 and L0596: 1. | | | |
| 81 | HAGDN53 | 1092161 | 91 | 2 - 430 | 704 | Ala-1 to Met-18, Leu-20 to Asn-26, Val-38 to Leu-46, Pro-48 to Gly-53, Leu-81 to Gly-86, Gln-94 to Tyr-99, Glu-101 to Gly-109. | AR050: 17, AR051: 11, AR054: 2, AR089: 1, AR061: 0 S0010: 1 and S0027: 1. | | | |
| 82 | HAMFM39 | 971347 | 92 | 1121 - 2929 | 705 | Pro-9 to Gln-16, Phe-31 to Tyr-40, Gln-61 to Trp-66, Arg-71 to Gln-78, Gly-86 to Arg-92. Gln-1 to Ala-7, Thr-36 to Trp-42, Gly-45 to Gly-52, Glu-77 to Pro-89, Gly-105 to Gly-132, Ser-135 to Glu-162. | AR050: 193, AR054: 122, AR051: 84, AR089: 0, AR061: 0 H0255: 59, H0254: 10, H0617: 9, L0747: 8, S0358: 7, H0486: 6, L0655: 6, H0208: 4. | | | |

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| 83 | HBGQT03 | 908173 | 93 | 3 - 791 | 706 | Lys-1 to Ala-15, Glu-22 to Val-31, Glu-37 to Thr-48, Leu-143 to Asp-160, Thr-170 to Ala-201, Ala-214 to Asp-219. | AR061: 6, AR089: 3 H0617: 10, L0665: 4, H0333: 3, S0366: 3, L0759: 3, H0599: 2, L0648: 2, L0653: 2, L0664: 2, H0519: 2, H0686: 1, H0484: 1, H0664: 1, H0392: 1, L0622: 1, S0280: 1, H0545: 1, T0010: 1, H0424: 1, H0031: 1, | | | | |

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| 84 | HBGSJ13 | 1150790 | 94 | 822 - 1 | 707 | | | | AR089: 1, AR061: 0 H0617: 2, H0013: 1, H0271: 1, L0455: 1 and H0539: 1. | | | |
| | | 878322 | 510 | 1 - 684 | 1123 | | | | | | | |
| 85 | HBIBQ89 | 909782 | 95 | 2 - 577 | 708 | | | | AR089: 1, AR061: 0 L0438: 6, L0751: 6, L0439: 5, L0770: 4, H0052: 2, H0620: 2, H0521: 2, L0756: 2, L0731: 2, L0758: 2, L0588: 2, H0556: 1, S0282: 1, H0662: 1, H0402: 1, S0418: 1, T0008: 1, S0222: 1, H0392: 1, H0333: 1, | | | |

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| | | | | | | | | | L0021: 1, H0581: 1, S0049: 1, L0471: 1, H0266: 1, L0351: 1, L0772: 1, L0766: 1, L0776: 1, L0659: 1, L0792: 1, H0522: 1, S0027: 1, L0779: 1 and S0011: 1. | | | |
| 86 | HCECM90 | 945088 | 96 | 2 - 577 | 709 | Gly-12 to Gly-31, Asn-38 to Gly-62, Asp-70 to Phe-84, Val-94 to Ser-101, Ala-112 to Ser-125, Lys-140 to Asn-145, Asn-175 to Tyr-180, Arg-187 to Thr-192. | | | AR061: 2, AR089: 1 H0013: 3, L0439: 2, H0624: 1, H0171: 1, S0040: 1, S0420: 1, H0619: 1, H0156: 1, H0575: 1, H0590: 1, H0052: 1, H0011: 1, H0266: 1, H0494: 1, L0519: 1, H0519: 1, H0555: 1, L0777: 1, L0758: 1, S0436: 1 and H0506: 1. | | | |
| 87 | HCEPH71 | 522739 | 97 | 3 - 410 | 710 | Val-1 to Lys-8, Pro-36 to Lys-41, Gln-49 to Lys-57, Ser-63 to Ser-70, Asp-79 to Gln-92, Asn-103 to Thr-122. | | | AR089: 1, AR061: 1 H0052: 1 and T0067: 1. | | | |

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| 88 | HCFMT57 | 1175204 | 98 | 3 - 1220 | 711 | Arg-4 to Val-12, Glu-19 to Arg-29, Glu-34 to Arg-76. | AR061: 0, AR089: 0 L0157: 2, H0620: 2, L0666: 2, S0001: 1, L0717: 1, H0549: 1, S0222: 1, H0581: 1, H0194: 1, H0015: 1, H0399: 1, H0271: 1, H0688: 1, H0428: 1, H0124: 1, L0637: 1, H0672: 1, L0439: 1, L0750: 1 and H0423: 1. | | |
| | | 765375 | 511 | 380 - 3 | 1124 | Glu-5 to Arg-15, Glu-20 to Arg-62. | | | |
| 89 | HCOMM05 | 1173146 | 99 | 3 - 851 | 712 | Gln-22 to Asp-41, Pro-49 to Thr-58, Leu-99 to Gly-107, Ala-117 to Ala-122, Gln-128 to Trp-134, Pro-136 to Pro-144, Phe-147 to Glu-153, Glu-183 to Val-188, Glu-195 to Glu-200, Glu-257 to Leu-265, Met-275 to Ser-283. | AR089: 1, AR061: 1 H0670: 1 | | |
| | | 925952 | 512 | 1 - 840 | 1125 | Gln-19 to Asp-38, Pro-46 to Thr-55, | | | |

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| | | 911386 | 513 | 3 - 428 | 1126 | Asp-1 to Glu-11, Ala-22 to Lys-28, Glu-42 to Leu-61, Arg-78 to Cys-90, Leu-97 to Glu-103. | L0596: 1, L0601: 1, H0542: 1 and H0543: 1. | | |
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| 93 | HDPDA47 | 929193 | 103 | 103 - 906 | 716 | Arg-17 to Leu-34, Asp-44 to Ser-51, Asp-63 to Gly-72, Pro-74 to Gly-83, Thr-97 to Met-102. | AR089: 11, AR061: 3 H0521: 7, H0581: 3, H0422: 3, H0650: 2, H0486: 2, S0002: 2, L0770: 2, L0769: 2, L0766: 2, L0518: 2, L0783: 2, L0777: 2, L0731: 2, H0445: 2, H0556: 1, H0583: 1, H0657: 1, H0656: 1, H0341: 1, H0575: 1, H0457: 1, H0179: 1, H0271: 1, L0055: 1, H0264: 1, H0488: 1, S0426: 1, L0662: 1, L0775: 1, L0655: 1, L0665: 1, S0053: 1, H0702: 1, H0701: 1, H0659: 1, L0754: 1, | | |

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| 94 | HDPFF24 | 909232 | 104 | 104 - 460 | 717 | | L0779: 1, L0759: 1 and H0543: 1. | | |
| | | | | | | | AR089: 4, AR061: 1 H0171: 5, S0026: 3, S0400: 2, L0471: 2, H0031: 2, H0553: 2, H0547: 2, H0521: 2, L0759: 2, H0423: 2, H0170: 1, H0583: 1, H0656: 1, S0001: 1, S0358: 1, S0360: 1, H0244: 1, H0349: 1, H0590: 1, H0310: 1, H0014: 1, H0039: 1, S0366: 1, H0551: 1, L0351: 1, H0509: 1, S0150: 1, L0369: 1, L0796: 1, L0773: 1, L0662: 1, L0766: 1, L0803: 1, L0635: 1, L0540: 1, H0519: 1, H0684: 1, H0660: 1, H0666: 1, S0044: 1, H0478: 1, H0479: 1, H0626: 1, L0748: 1, L0740: 1, L0777: 1, | | |

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| 95 | HDPPO35 | 966248 | 105 | 72 - 1202 | 718 | Lys-7 to Gly-69, Lys-82 to Lys-88, Ser-94 to Asp-112, Ala-126 to Asp-131, Tyr-134 to Ser-140, Ser-147 to Phe-156, Asp-159 to Ser-165, Thr-176 to Asp-186, Glu-230 to Leu-250, Glu-291 to Arg-298, Gln-313 to Glu-320, Asn-331 to Gly-343, Ser-348 to Leu-363. | L0752: 1, L0755: 1 and H0543: 1. AR089: 1, AR061: 0 H0521: 15, H0638: 5, H0580: 5, H0271: 5, H0641: 5, H0560: 4, H0090: 3, H0591: 3, L0766: 3, H0542: 3, H0543: 3, H0586: 2, H0497: 2, H0581: 2, L0655: 2, H0518: 2, H0522: 2, L0754: 2, L0747: 2, H0657: 1, H0393: 1, H0431: 1, H0250: 1, H0635: 1, L0021: 1, H0014: 1, H0179: 1, H0416: 1, H0488: 1, L0475: 1, H0359: 1, H0625: 1, S0426: 1, L0598: 1, L0667: 1, L0803: 1, L0804: 1, L0775: 1, L0651: 1, L0659: 1, L0792: 1, L0663: 1, S0428: 1, H0672: 1, H0555: 1, H0436: 1, | | |
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| 96 | HDPSR74 | 911396 | 106 | 212 - 583 | 719 | Leu-31 to Ser-39, Val-57 to Trp-63, Pro-103 to Gln-111, Leu-118 to Leu-124. | L0779: 1, H0445: 1 and S0424: 1. AR050: 48, AR054: 42, AR051: 35, AR089: 3, AR061: 1 H0575: 2, H0580: 1, S0002: 1, S0426: 1, H0521: 1, H0436: 1 and L0748: 1. | | |
| 97 | HDTKQ14 | 886936 | 107 | 1 - 555 | 720 | Ser-60 to Thr-71, Thr-82 to Leu-94, Gln-113 to Asp-123, Val-125 to Tyr-133, Leu-144 to Gly-149. | AR054: 60, AR051: 40, AR050: 36, AR089: 5, AR061: 2 H0521: 4, H0486: 2, S0002: 2, L0770: 2, L0769: 2, L0766: 2, L0518: 2, L0783: 2, L0777: 2, L0731: 2, H0422: 2, H0556: 1, H0583: 1, H0650: 1, H0657: 1, H0179: 1, L0055: 1, H0488: 1, S0426: 1, L0662: 1, L0775: 1, L0655: 1, L0665: 1, S0053: 1, H0659: 1, L0754: 1, L0779: 1, L0759: 1 and | | |

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| 98 | HE6GF02 | 1150897 | 108 | 804 - 1 | 721 | Gln-13 to Ser-18, Glu-32 to Gly-37, Ala-44 to Trp-49, Glu-56 to Val-61, Gln-68 to Lys-74, Ala-83 to Glu-88, Arg-111 to Gly-117, Tyr-123 to His-143, Ser-167 to Thr-202. | H0543: 1. AR061: 7, AR089: 4 H0100: 1 and H0521: 1. | | |
| | | 911263 | 514 | 1 - 264 | 1127 | Gln-13 to Ser-18, Glu-32 to Gly-37, Ala-44 to Trp-49. | | | |
| 99 | HE8PK12 | 909884 | 109 | 2 - 367 | 722 | Val-30 to Ser-37, Gln-43 to Asp-62, Pro-74 to Glu-79, Thr-102 to Phe-109. | AR089: 6, AR061: 4 L0754: 6, L0777: 6, L0740: 5, L0731: 4, L0758: 4, L0759: 4, S0001: 3, S0280: 3, L0770: 3, L0764: 3, L0747: 3, L0749: 3, L0366: 3, S0412: 3, S0007: 2, H0411: 2, H0013: 2, L0471: 2, T0004: 2, L0598: 2, L0638: 2, L0662: 2, L0783: 2, L0438: 2, | | |

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| | | | | | | | | H0696: 2, L0744: 2, L0748: 2, L0751: 2, L0745: 2, L0779: 2, L0752: 2, H0170: 1, S0282: 1, H0662: 1, H0574: 1, T0060: 1, H0427: 1, H0590: 1, S0010: 1, L0105: 1, S0049: 1, H0194: 1, H0373: 1, L0163: 1, H0201: 1, H0031: 1, H0553: 1, S0306: 1, L0776: 1, L0659: 1, L0526: 1, L0809: 1, L0663: 1, H0144: 1, H0547: 1, H0648: 1, H0672: 1, L0743: 1, L0780: 1, S0031: 1, H0343: 1, L0604: 1 and H0653: 1. | | |
| 100 | HE9SE62 | 911476 | 110 | 1 - 564 | 723 | | | AR061: 16, AR089: 6 L0804: 1, S0052: 1, H0144: 1 and H0659: 1. | | |
| 101 | HEOPL36 | 1195682 | 111 | 86 - 487 | 724 | Gly-11 to Thr-16, Ser-35 to Ser-56, Thr-58 to Ser-73, | | AR089: 18, AR061: 5 L0740: 11, L0439: 9, L0748: 8, H0616: 5, | | |

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| | | | | | | | H0024: 1, T0010: 1, H0510: 1, H0644: 1, S0036: 1, H0551: 1, H0264: 1, H0488: 1, H0056: 1, H0100: 1, L0564: 1, T0041: 1, H0652: 1, S0344: 1, S0002: 1, L0763: 1, L0638: 1, L0761: 1, L0372: 1, L0643: 1, L0764: 1, L0768: 1, L0381: 1, L0775: 1, L0526: 1, L0782: 1, L0663: 1, L0665: 1, H0703: 1, H0520: 1, H0435: 1, H0521: 1, S0044: 1, L0751: 1, L0757: 1, L0759: 1, H0445: 1, L0584: 1, L0608: 1 and H0506: 1. | | |
| 102 | HFBDJ13 | 911264 | 968826 | 515 | 85 - 486 | 1128 | Gly-11 to Thr-16, Ser-35 to Ser-56, Thr-58 to Ser-73, Tyr-85 to Asp-91, Glu-100 to Glu-109. Ser-6 to Trp-24. | S0007: 2, L0794: 2, | |

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| | | | | | | L0617: 1, S0358: 1, H0609: 1, H0592: 1, H0333: 1, T0040: 1, H0013: 1, H0635: 1, H0575: 1, H0036: 1, H0581: 1, H0123: 1, H0050: 1, H0012: 1, H0071: 1, T0010: 1, H0687: 1, H0290: 1, H0617: 1, H0606: 1, H0038: 1, H0487: 1, H0494: 1, H0334: 1, S0150: 1, H0647: 1, S0142: 1, L0640: 1, L0639: 1, L0637: 1, L0641: 1, L0768: 1, L0649: 1, L0514: 1, L0659: 1, L0783: 1, L0788: 1, L0664: 1, L0665: 1, L0438: 1, H0547: 1, H0435: 1, H0522: 1, H0696: 1, S0404: 1, H0478: 1, L0742: 1, L0740: 1, L0749: 1, L0758: 1, S0434: 1, S0194: 1, | | | | | |
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| 106 | HIIDS62 | 935932 | 116 | 1 - 519 | 729 | Ser-11 to Trp-16, Ile-20 to Trp-26, Asn-37 to Ser-58, Leu-67 to Gln-72, Lys-101 to Asp-108, Asp-135 to Tyr-140. | H0422: 1 and H0506: 1, AR089: 2, AR061: 1 T0049: 1, S0278: 1, H0031: 1 and H0539: 1. | | |
| 107 | HLQDT35 | 839777 | 117 | 222 - 494 | 730 | | AR089: 3, AR061: 3 S0358: 8, L0766: 7, L0777: 7, L0731: 7, L0659: 4, L0748: 4, L0751: 4, L0783: 3, L0663: 3, S0418: 2, S0360: 2, H0486: 2, S0010: 2, S0250: 2, S0422: 2, L0763: 2, L0803: 2, L0775: 2, L0789: 2, H0520: 2, L0756: 2, L0752: 2, H0656: 1, S0376: 1, H0208: 1, H0574: 1, H0632: 1, S0414: 1, H0581: 1, H0052: 1, H0024: 1, H0014: 1, H0355: 1, H0688: 1, H0090: 1, H0623: 1, | | |

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| 109 | HMEFT66 | 856149 | 119 | 2 - 349 | 732 | | | | AR061: 1, AR089: 1 H0175: 1, H0266: 1, H0292: 1, H0628: 1 and L0779: 1. | | | | | |
| 110 | HMSCD15 | 918133 | 120 | 237 - 635 | 733 | | | | AR089: 1, AR061: 1 S0002: 2 and L0766: 1. | | | | | |

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| 111 | HMSHO64 | 746582 | 121 | 1 - 411 | 734 | Ser-11 to Ser-21, Ser-84 to Ala-89, Pro-98 to Arg-107. | AR089: 2, AR061: 2 S0002: 2 | | |
| 112 | HMTAW83 | 911385 | 122 | 1 - 363 | 735 | Ile-26 to Trp-33, Glu-52 to Leu-71. | AR089: 0, AR061: 0 H0583: 1, H0644: 1, L0766: 1 and H0518: 1. | | |
| 113 | HMVAM09 | 963814 | 123 | 2 - 802 | 736 | | AR089: 4, AR061: 1 L0731: 7, L0517: 5, S0212: 3, L0775: 3, L0740: 3, H0266: 2, L0809: 2, H0696: 2, L0748: 2, S0132: 1, H0574: 1, H0013: 1, H0544: 1, H0023: 1, H0071: 1, H0286: 1, H0100: 1, H0494: 1, S0370: 1, L0770: 1, L0646: 1, L0764: 1, L0771: 1, L0363: 1, L0774: 1, L0659: 1, L0789: 1, L0666: 1, S0126: 1, H0522: 1, L0754: 1, L0747: 1 and L0755: 1. | | |
| 114 | HNSAA28 | 946988 | 124 | 85 - 1557 | 737 | Glu-9 to Ser-20, Ile-23 to Gly-29, | AR050: 8, AR054: 6, AR051: 3, AR089: 1, | | |

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| | | | | | | Pro-50 to Cys-66, Pro-74 to Glu-79, Glu-93 to Trp-98, Thr-121 to Ser-133, Leu-180 to Lys-196, Thr-213 to Glu-225, Glu-234 to Glu-240, Arg-263 to Glu-270, Glu-283 to Ala-298, Lys-318 to Ala-336, Val-340 to Ala-351, Val-361 to Pro-372, Asn-445 to Pro-468, Pro-475 to Lys-491. | | | | AR061: 1 H0036: 2, L0766: 2, H0686: 1, H0622: 1, H0625: 1, L0791: 1, L0779: 1 and S0434: 1. | |
| | | 972348 | 516 | 3 - 452 | 1129 | Thr-1 to Ala-10, Val-20 to Pro-31, Asn-104 to Thr-124. | | | | | |
| 115 | HOGEQ43 | 1226207 | 125 | 494 - 2083 | 738 | Lys-1 to Thr-34, Phe-80 to Gly-85, Tyr-91 to Ser-105, Thr-122 to Ala-133, Ser-151 to Ala-157, Glu-208 to Trp-213, His-219 to Trp-224, Glu-237 to Glu-244, Asn-251 to Ser-256, | | | | AR089: 1, AR061: 0 H0457: 8, L0766: 7, L0599: 6, H0677: 6, L0438: 5, L0779: 5, H0012: 3, L0809: 3, H0656: 2, H0620: 2, L0771: 2, H0435: 2, H0436: 2, L0748: 2, L0439: 2, L0751: 2, | |

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| 116 | HOUDHI9 | 935465 | 517 | 1 - 150 | 1130 | Gln-291 to Trp-296, Asn-311 to Phe-321, Ser-327 to Glu-335, Lys-364 to Trp-369, Ala-376 to Gly-384, Asn-437 to Trp-444, Met-462 to Trp-472, Gln-483 to Gly-491, Thr-499 to Trp-504, Arg-512 to Ala-517. | L0749: 2, S0134: 1, H0645: 1, H0587: 1, H0635: 1, H0581: 1, H0546: 1, H0477: 1, H0560: 1, H0641: 1, S0422: 1, H0529: 1, L0521: 1, L0662: 1, L0794: 1, L0774: 1, L0775: 1, L0606: 1, L0659: 1, L0647: 1, L0789: 1, L0791: 1, L0792: 1, L0666: 1, L0663: 1, L0665: 1, H0702: 1, H0547: 1, H0576: 1, S0028: 1, L0756: 1, L0777: 1, L0755: 1, L0758: 1, H0543: 1 and H0506: 1. | | |
| | | | | | | Glu-1 to Thr-13. | | | |
| | | | | | | Pro-8 to Ser-13. | | | |
| | | | | | | Thr-8 to Gln-19, | | | |
| 116 | HOUDHI9 | 1150918 | 126 | 506 - 3 | 739 | AR089: 1, AR061: 0 S0040: 1, H0250: 1, T0048: 1, L0761: 1, L0764: 1, L0783: 1, L0809: 1, L0789: 1 and L0757: 1. | | | |
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| 116 | HOUDHI9 | 908588 | 518 | 52 - 573 | 1131 | Thr-8 to Gln-19, | | | |
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| 117 | HOUFT36 | 911293 | 127 | 160 - 846 | 740 | Lys-26 to Glu-33, Lys-41 to Ile-50. Lys-27 to Ile-43. | AR089: 2, AR061: 1 L0794: 6, L0598: 2, L0803: 2, L0748: 2, S0040: 1, S0046: 1, H0431: 1, H0318: 1, L0766: 1, L0606: 1, L0749: 1, L0758: 1 and S0192: 1. | | |
| 118 | HPMFL08 | 959569 | 128 | 191 - 346 | 741 | Met-43 to Trp-52. | AR089: 1, AR061: 1 H0031: 2 | | |
| 119 | HRSMD49 | 723025 | 129 | 190 - 456 | 742 | Gln-36 to Ile-46, Ser-55 to Phe-65, Ser-67 to Lys-78. | AR089: 3, AR061: 2 H0394: 1 and L0589: 1. | | |
| 120 | HSDII69 | 917180 | 130 | 202 - 540 | 743 | His-13 to Gly-21, Tyr-61 to Asp-66, Ala-105 to Thr-110. | AR061: 6, AR089: 5 H0328: 4, H0031: 3, L0519: 3, L0748: 2, L0777: 2, L0731: 2, S0260: 2, H0624: 1, S6024: 1, H0650: 1, S0116: 1, H0254: 1, S0007: 1, H0393: 1, H0441: 1, H0438: 1, H0574: 1, H0156: 1, H0599: 1, S0051: 1, | | |

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| 121 | HSDSB06 | 949151 | 131 | 3 - 863 | 744 | Ile-25 to Asn-36, Glu-54 to Val-63, Gly-81 to Glu-86, Gly-108 to Thr-114, Val-125 to Ser-131. | H0615: 1, H0039: 1, L0564: 1, L0763: 1, L0766: 1, L0774: 1, L0776: 1, L0659: 1, L0518: 1, L0792: 1, L0666: 1, L0663: 1, S0242: 1 and H0423: 1. AR061: 4, AR089: 3 H0590: 7, L0754: 5, H0156: 3, L0731: 3, L0600: 3, S0360: 2, H0339: 2, S0472: 2, L0803: 2, L0751: 2, L0779: 2, L0759: 2, S0031: 2, L0596: 2, S0212: 1, H0411: 1, S0222: 1, H0409: 1, H0601: 1, H0333: 1, H0632: 1, H0427: 1, L0021: 1, H0037: 1, H0596: 1, H0024: 1, H0239: 1, S0628: 1, H0266: 1, H0687: 1, H0328: 1, H0644: 1, H0674: 1, H0598: 1, T0067: 1, H0509: 1, | | |
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| | | | | | | | | | L0763: 1, L0772: 1, L0764: 1, L0771: 1, L0773: 1, L0650: 1, L0806: 1, L0659: 1, L0547: 1, L0809: 1, L0666: 1, L0663: 1, L0665: 1, S0328: 1, S0380: 1, S0390: 1, S0032: 1, L0744: 1, L0745: 1, L0746: 1, L0747: 1, L0756: 1, L0777: 1, L0758: 1, L0588: 1, S0276: 1, S0196: 1, S0412: 1 and H0506: 1. | | | |
| 122 | HSFAM09 | 1150965 | 132 | 2 - 325 | 745 | Leu-2 to Gly-8. | AR061: 5, AR089: 2 H0154: 2 | | | | | |
| | | 573345 | 519 | 147 - 332 | 1132 | Arg-1 to Ser-8, Lys-42 to Lys-48. | | | | | | |
| 123 | HSSAX53 | 507509 | 133 | 209 - 361 | 746 | | H0135: 1 and H0063: 1. | | | | | |
| 124 | HSVAV49 | 1150960 | 134 | 220 - 486 | 747 | Pro-19 to Thr-24, Thr-78 to Lys-89. | AR061: 9, AR089: 7 H0309: 1 | | | | | |
| | | 689674 | 520 | 44 - 208 | 1133 | Glu-21 to Glu-27. | | | | | | |
| 125 | HTEAG49 | 954614 | 135 | 510 - 208 | 748 | | AR089: 1, AR061: 0 L0759: 4, L0770: 2, | | | | | |

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| 126 | HTLBH67 | 751985 | 136 | 1 - 282 | 749 | | | | S0040: 1, S0318: 1, S0334: 1, S0316: 1, S0340: 1, H0038: 1, L0598: 1, L0800: 1 and S0276: 1. | | |
| | | | | | | | | | AR061: 2, AR089: 1 L0752: 3, L0747: 2, H0294: 1, H0253: 1, H0046: 1, H0040: 1, H0063: 1, H0494: 1, S0352: 1, L0769: 1, L0766: 1, L0804: 1, L0805: 1, L0791: 1, H0521: 1, L0779: 1, L0780: 1, L0731: 1 and L0758: 1. | | |
| 127 | HTLJC71 | 922923 | 137 | 3 - 1355 | 750 | | | His-1 to Phe-9, Cys-13 to Thr-18, Pro-35 to Gly-48, Glu-61 to Pro-68, Lys-105 to Ala-136, Thr-144 to Gln-154, Leu-163 to Gly-171, Thr-205 to Gln-222, Pro-251 to Gln-257. | AR061: 7, AR089: 5 H0618: 12, H0253: 8, H0038: 6, L0758: 6, L0779: 5, H0616: 3, T0041: 1, L0776: 1, S0274: 1 and H0543: 1. | | |
| 128 | HTPAD46 | 503313 | 138 | 103 - 309 | 751 | | | His-50 to Leu-69. | AR061: 0, AR089: 0 | | |

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| | | | | | | | | | L0794: 4, H0039: 2, S0358: 1, H0013: 1, H0575: 1, L0770: 1, L0769: 1 and L0749: 1. | | |
| 129 | HTTKP07 | 911390 | 139 | 2 - 337 | 752 | Thr-15 to Asp-25, Glu-69 to Leu-89. | | | AR089: 1, AR061: 1 H0634: 2 | | |
| 130 | HUCOW17 | 933357 | 140 | 155 - 856 | 753 | Gln-27 to Trp-45. | | | AR089: 4, AR061: 2 L0439: 5, S0002: 3, L0604: 3, H0619: 2, H0024: 2, H0625: 2, L0768: 2, L0757: 2, H0638: 1, S0420: 1, S0360: 1, H0586: 1, L0163: 1, S0214: 1, L0143: 1, H0264: 1, L0769: 1, L0764: 1, L0774: 1, L0651: 1, L0659: 1, L0542: 1, L0789: 1, H0539: 1, H0521: 1, S0044: 1, L0777: 1, L0758: 1, L0599: 1 and H0422: 1. | | |
| 131 | HWHGF52 | 726102 | 141 | 1 - 453 | 754 | Gln-1 to Lys-8, Gly-10 to Trp-17, Val-28 to Gly-43, Thr-54 to Glu-63. | | | AR089: 1, AR061: 0 L0776: 5, L0764: 4, L0743: 4, L0740: 3, L0750: 3, L0777: 3, | | |

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| 132 | HWHHB69 | 1212612 | 142 | 2 - 2176 | 755 | Gly-1 to Ser-7. | AR089: 1, AR061: 1 |
| | | | | | | | S0434: 1 and L0595: 1. |
| | | | | | | | L0731: 3, S0001: 2, H0438: 2, H0052: 2, H0194: 2, H0201: 2, L0526: 2, H0144: 2, L0742: 2, H0662: 1, H0619: 1, H0261: 1, H0392: 1, H0455: 1, H0586: 1, H0587: 1, H0574: 1, H0486: 1, H0013: 1, H0427: 1, S0010: 1, S0346: 1, T0110: 1, H0009: 1, L0157: 1, H0320: 1, H0051: 1, T0006: 1, H0604: 1, H0163: 1, H0646: 1, L0763: 1, L0638: 1, L0630: 1, L0646: 1, L0773: 1, L0651: 1, L0523: 1, L0805: 1, L0666: 1, L0663: 1, L0664: 1, H0547: 1, H0660: 1, S0404: 1, L0744: 1, L0439: 1, L0752: 1, |
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| | | | | | Ala-70 to Tyr-77, Arg-130 to Ser-140. | L0803: 3, S0354: 2, H0052: 2, H0617: 2, L0770: 2, L0646: 2, S0028: 2, L0753: 2, H0445: 2, H0556: 1, S6024: 1, H0657: 1, S0418: 1, S0420: 1, H0351: 1, H0441: 1, H0586: 1, H0013: 1, S0280: 1, H0156: 1, L0021: 1, H0122: 1, S0010: 1, H0571: 1, L0163: 1, H0135: 1, H0412: 1, H0100: 1, L0351: 1, L0769: 1, L0639: 1, L0764: 1, L0649: 1, L0659: 1, L0809: 1, L0530: 1, H0520: 1, H0547: 1, H0519: 1, H0690: 1, H0539: 1, S0136: 1, H0696: 1, L0748: 1, L0747: 1, L0756: 1, L0779: 1, L0757: 1, S0434: 1, S0436: 1, S0011: 1 and H0136: 1. | | |
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| | | 690442 | 521 | 1 - 261 | 1134 | Gly-1 to Ser-7. | | | |
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| 133 | HWLFH94 | 1151387 | 143 | 695 - 333 | 756 | | AR089: 5, AR061: 2 S0358: 5, L0596: 3, L0771: 2, L0758: 2, S0354: 1, S0376: 1, T0109: 1, H0036: 1, H0590: 1, L0040: 1, H0038: 1, H0616: 1, L0646: 1, L0764: 1, L0768: 1, L0775: 1, L0659: 1 and S0404: 1. | | |
| | | 909682 | 522 | 134 - 535 | 1135 | Ser-25 to Ala-52, Phe-64 to Glu-71. | | | |
| 134 | HWMBM13 | 909683 | 144 | 3 - 539 | 757 | Pro-11 to Ala-35, Phe-47 to Glu-54, Glu-78 to Gly-83, Gln-94 to Ser-106, Ser-114 to Val-120. | AR089: 2, AR061: 2 S0358: 6, L0794: 4, L0758: 4, S0354: 3, L0779: 3, L0596: 3, S0376: 2, H0036: 2, H0620: 2, H0063: 2, L0771: 2, L0803: 2, L0654: 2, L0659: 2, T0109: 1, H0013: 1, H0590: 1, H0052: 1, H0596: 1, T0110: 1, L0040: 1, H0090: 1, H0038: 1, H0040: 1, | | |

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| 135 | HWWDN34 | 911357 | 145 | 2 - 1000 | 758 | Ser-11 to Leu-17, Pro-20 to Val-26, Ser-87 to Lys-95, Thr-109 to Lys-116, Pro-164 to Gln-170, Glu-222 to Ser-227, Ser-292 to Gln-303, Asp-315 to Gly-324, Gly-326 to Ala-333. | AR089: 1, AR061: 1 S0354: 16, H0457: 7, L0758: 3, H0555: 2, H0170: 1, H0657: 1, H0255: 1, H0662: 1, S0360: 1, H0036: 1, H0150: 1, H0051: 1, H0553: 1, L0800: 1, L0644: 1, L0771: 1, L0803: 1, L0787: 1, L0663: 1, H0144: 1, S0374: 1, H0670: 1, H0522: 1, L0749: 1, S0452: 1 and H0506: 1. | H0616: 1, H0429: 1, H0561: 1, L0646: 1, L0764: 1, L0768: 1, L0766: 1, L0775: 1, L0790: 1, L0792: 1, S0404: 1, S0390: 1, L0777: 1, L0755: 1, L0592: 1 and S0458: 1. | | |
| 136 | HCEML27 | 997051 | 146 | 750 - 61 | 759 | Pro-93 to Asp-102, Pro-112 to Ala-119, Ser-131 to Pro-150, Glu-188 to Gly-196. | AR061: 1, AR089: 1 L0761: 4, L0439: 4, L0758: 4, L0769: 3, L0771: 3, L0662: 3, | | | |

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| 137 | HELHJ69 | | | | | | | L0666: 3, L0665: 3, L0741: 3, L0743: 3, H0559: 2, H0318: 2, H0266: 2, L0776: 2, L0809: 2, L0664: 2, L0740: 2, L0747: 2, L0750: 2, L0757: 2, S0356: 1, H0587: 1, H0581: 1, H0052: 1, H0545: 1, H0086: 1, H0620: 1, L0119: 1, H0039: 1, L0637: 1, L0800: 1, L0764: 1, L0803: 1, L0655: 1, L0657: 1, L0659: 1, L0636: 1, L0782: 1, L0663: 1, H0520: 1, S0044: 1, L0748: 1, L0754: 1, L0779: 1, L0755: 1, L0731: 1, L0592: 1, S0276: 1, H0677: 1 and S0456: 1. | AR061: 3, AR089: 1 | | |
| | | 771667 | 523 | 2 - 355 | 1136 | Gln-19 to Glu-26, Phe-33 to Lys-38, Asn-45 to Val-52. | | | | | |
| | | 1128924 | 147 | 18 - 596 | 760 | Ala-7 to Lys-19, | | | | | |

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| | | | | | Gly-30 to Gly-35, Ser-50 to Glu-61, Ala-74 to Pro-81. | H0254: 2, H0255: 2, S0045: 2, H0266: 2, H0052: 1, H0050: 1, H0063: 1, H0488: 1 and H0423: 1. | | |
| | 911262 | 524 | 1 - 597 | 1137 | Pro-9 to Lys-25, Gly-36 to Gly-41, Ser-56 to Glu-67, Ala-80 to Pro-87. | | | |
| 138 | HFKLA09 | 117800 | 148 | 3 - 1574 | 761 | His-1 to Asp-11, Val-33 to Pro-57, Gly-68 to Glu-74, Pro-76 to Pro-81, Phe-93 to Val-120, Pro-131 to Pro-146, Pro-161 to Pro-168, Tyr-178 to Ser-184, Pro-187 to Gly-215, Asn-229 to Asn-244, Asp-250 to Trp-255, Pro-258 to Asp-263, Pro-300 to Val-310, Asp-364 to Glu-371, Thr-441 to Lys-446, Ser-462 to Thr-477, Lys-487 to Trp-492. | AR061: 4, AR089: 2, L0777: 11, L0748: 10, L0803: 8, L0794: 7, L0750: 6, H0620: 5, L0749: 5, H0622: 4, L0805: 4, L0809: 4, L0665: 4, H0550: 3, H0575: 3, H0023: 3, L0659: 3, L0790: 3, S0356: 2, H0549: 2, S0222: 2, H0592: 2, H0427: 2, L0157: 2, H0213: 2, L0763: 2, L0662: 2, L0774: 2, L0789: 2, L0666: 2, H0539: 2, L0743: 2, L0744: 2, L0600: 2, | |

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| | | 952634 | 525 | 2 - 1567 | 1138 | Thr-2 to Asp-9, Val-31 to Pro-55, Gly-66 to Glu-72, Pro-74 to Pro-79, Phe-91 to Val-118, Pro-129 to Pro-144. | | | | |
| 139 | HSBBF79 | 965764 | 149 | 3 - 707 | 762 | Gln-2 to Glu-12. | AR061: 520, AR089: 428 S0040: 1, H0669: 1, H0662: 1, S0420: 1, S0358: 1, S0376: 1, H0632: 1, T0040: 1, T0110: 1, H0633: 1, L0800: 1, H0666: 1, S0152: 1, S0028: 1, L0581: 1 and L0594: 1. | | | |
| 140 | HSLKA77 | 1204269 | 150 | 22 - 1137 | 763 | | AR061: 4, AR089: 3 L0748: 20, L0731: 8, L0755: 6, H0031: 5, H0644: 5, H0090: 5, L0775: 5, L0749: 5, S0360: 4, L0770: 4, L0766: 4, L0740: 4, L0754: 4, L0777: 4, L0757: 4, L0758: 4, H0050: 3, L0764: 3, | | | |

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| | | L0768: 3, L0666: 3, L0665: 3, L0750: 3, L0756: 3, S0212: 2, H0580: 2, H0545: 2, H0123: 2, L0471: 2, H0012: 2, S0022: 2, H0622: 2, H0553: 2, H0383: 2, S0344: 2, L0662: 2, L0657: 2, L0663: 2, L0664: 2, H0144: 2, H0555: 2, S0390: 2, L0743: 2, L0747: 2, L0759: 2, L0581: 2, L0599: 2, H0265: 1, H0295: 1, T0049: 1, S0358: 1, H0619: 1, L0717: 1, H0592: 1, H0486: 1, L0477: 1, T0039: 1, T0040: 1, H0013: 1, S0010: 1, H0318: 1, H0052: 1, H0046: 1, H0023: 1, H0051: 1, T0079: 1, H0355: 1, H0510: 1, H0290: 1, S0250: 1, H0628: 1, |
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| 141 | hagdr21 | 911589 | 526 | 88 - 414 | 1139 | Pro-52 to Asp-57, Asp-67 to Trp-72, Lys-87 to Gly-92, Asp-98 to Gly-104. | L0456: 1, H0316: 1, H0040: 1, H0264: 1, H0623: 1, H0494: 1, S0016: 1, S0210: 1, L0761: 1, L0771: 1, L0650: 1, L0774: 1, L0375: 1, L0784: 1, L0776: 1, L0655: 1, H0547: 1, H0659: 1, H0670: 1, H0672: 1, H0696: 1, S0037: 1, S0028: 1, S0032: 1, L0744: 1, L0779: 1, L0752: 1, L0753: 1, S0031: 1 and L0366: 1. | | |
| | | 1090433 | 151 | 74 - 1183 | 764 | Gly-36 to Asp-42, Pro-51 to Ala-56, Gln-84 to Leu-91, His-105 to His-112, Tyr-115 to Pro-124, Pro-155 to Ser-162, Cys-167 to Ala-173, | AR061: 3, AR089: 1 S0222: 1, S6014: 1, S0010: 1, S6028: 1 and S0036: 1. | | |

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| 142 | HHFNH27 | 1025277 | 152 | 252 - 1634 | 765 | His-178 to Leu-190, Ser-217 to Ala-224, Pro-226 to Gly-234, Lys-270 to Ala-275, Pro-316 to Lys-323. Gly-10 to Asp-16, Pro-25 to Ala-30, Gln-58 to Leu-65. Arg-13 to Gly-21, Arg-24 to Gly-31, Ser-41 to Gln-73, Glu-83 to Gly-92, Asp-98 to Ala-103, Asn-105 to Gln-115, Glu-129 to Glu-135, Asp-142 to Gly-147, Val-149 to Met-154, His-171 to Lys-177, Pro-187 to Gly-196, Ala-199 to Cys-208, Arg-230 to Tyr-245, Glu-249 to His-256, Asn-265 to Phe-270, Val-277 to Arg-286, Ala-292 to Asp-300, Leu-327 to Pro-351. | AR089: 81, AR061: 32 H0341: 9, H0657: 7, S0358: 4, H0251: 4, H0428: 4, L0748: 4, L0750: 4, H0445: 4, S0116: 3, H0333: 3, H0318: 3, T0041: 3, S0126: 3, H0670: 3, H0648: 3, H0543: 3, H0170: 2, S0376: 2, S0360: 2, S0007: 2, H0619: 2, H0393: 2, H0486: 2, H0156: 2, H0596: 2, H0046: 2, H0014: 2, H0059: 2, T0004: 2, H0647: 2, L0521: 2, L0375: 2, L0517: 2, H0659: 2. | | |
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| | | | Gln-374 to His-380, Leu-382 to Gly-391, Lys-393 to Gly-402. | H0658: 2, H0660: 2, H0672: 2, S0380: 2, H0521: 2, S0044: 2, H0576: 2, L0747: 2, L0485: 2, L0595: 2, L0362: 2, S0026: 2, H0624: 1, S0180: 1, S0212: 1, H0663: 1, H0305: 1, H0459: 1, S0418: 1, S0420: 1, S0045: 1, S0046: 1, H0351: 1, S0222: 1, H0392: 1, H0249: 1, H0643: 1, H0331: 1, H0618: 1, T0071: 1, H0581: 1, H0421: 1, H0263: 1, L0040: 1, H0546: 1, H0009: 1, H0123: 1, H0050: 1, L0471: 1, H0012: 1, H0023: 1, H0015: 1, H0083: 1, H0510: 1, S0336: 1, H0687: 1, H0290: 1, H0028: 1, S0250: 1, S0022: 1, H0615: 1, T0006: 1, | |
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| | H0030: 1, H0169: 1, S0364: 1, H0068: 1, S0366: 1, H0376: 1, H0598: 1, H0090: 1, H0040: 1, H0412: 1, T0069: 1, L0564: 1, T0042: 1, H0494: 1, H0359: 1, H0646: 1, S0422: 1, H0026: 1, L0520: 1, L0625: 1, L0764: 1, L0767: 1, L0806: 1, L0655: 1, L0657: 1, L0809: 1, L0519: 1, L0789: 1, L0664: 1, S0374: 1, L0565: 1, H0689: 1, H0435: 1, H0414: 1, H0666: 1, H0539: 1, S0378: 1, S0004: 1, S0146: 1, S0027: 1, S0028: 1, S0206: 1, L0741: 1, L0439: 1, L0740: 1, L0754: 1, L0749: 1, L0756: 1, L0777: 1, L0731: 1, L0758: 1, L0581: 1, | | | | | | |
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| 143 | HTLIT05 | 1217625 | 153 | 81 - 623 | 766 | | | L0599: 1, L0608: 1, L0594: 1, L0603: 1, H0668: 1, H0665: 1, H0667: 1, S0194: 1, H0542: 1, H0423: 1, H0422: 1, S0424: 1 and H0506: 1. | | |
| 144 | HAPNV33 | 1151374 | 154 | 1 - 774 | 767 | | | AR061: 7, AR089: 2 H0619: 1, H0575: 1, H0615: 1 and S0028: 1. | | |
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| 145 | HBTAE84 | 1128800 | 155 | 3 - 416 | 768 | | | AR089: 1, AR061: 0 S0180: 1 | | |
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| 146 | HDPVY89 | 827026 | 156 | 2 - 580 | 769 | | | AR089: 4, AR061: 3 H0657: 3, H0253: 3, | | |
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| 147 | HGLDB21 | 1010920 | 157 | 240 - 1388 | 770 | Leu-20 to Pro-34, Lys-36 to Leu-55, Arg-63 to Gln-72, Pro-215 to Thr-222, Ile-288 to Leu-297, Ala-337 to Gly-346. | S0424: 1, H0506: 1 and H0008: 1. AR061: 10, AR089: 4 H0688: 2, L0803: 2, L0666: 2, L0749: 2, L0777: 2, L0594: 2, S0218: 1, H0657: 1, H0656: 1, H0341: 1, H0663: 1, H0351: 1, H0370: 1, H0318: 1, T0103: 1, H0024: 1, H0652: 1, L0769: 1, L0800: 1, L0794: 1, L0766: 1, L0561: 1, L0804: 1, L0657: 1, L0636: 1, L0635: 1, L0789: 1, L0663: 1, L0665: 1, L0750: 1 and H0216: 1. | | |
| | | 455474 | 531 | 3 - 230 | 1144 | Ala-30 to Gly-39. | | | |
| 148 | HMIAN37 | 947881 | 158 | 1 - 645 | 771 | Asp-60 to Lys-75, Glu-136 to Gln-142. | AR061: 2, AR089: 1 S0414: 26, L0439: 12, L0766: 10, L0779: 10, L0777: 10, L0758: 10, L0757: 8, L0752: 7, L0740: 5, H0170: 4, | | |

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| | | | | S0354: 4, L0471: 4, L0794: 4, L0653: 4, L0809: 4, L0666: 4, L0748: 4, H0441: 3, H0051: 3, H0266: 3, S0003: 3, H0644: 3, H0032: 3, L0770: 3, L0803: 3, L0664: 3, H0658: 3, S0380: 3, S3014: 3, S0206: 3, L0754: 3, L0750: 3, L0731: 3, S0192: 3, H0657: 2, S0298: 2, S0358: 2, S0360: 2, L0717: 2, S6016: 2, H0574: 2, T0040: 2, H0013: 2, H0052: 2, H0009: 2, S6028: 2, H0428: 2, H0090: 2, H0591: 2, S0422: 2, L0804: 2, L0659: 2, L0663: 2, L0665: 2, H0144: 2, H0689: 2, H0521: 2, S3012: 2, S0037: 2, S0028: 2, L0742: 2, L0745: 2, | | |
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| L0747: 2, L0756: 2, L0780: 2, L0753: 2, H0667: 2, H0423: 2, S0412: 2, H0171: 1, H0686: 1, S0040: 1, T0049: 1, H0656: 1, S0212: 1, H0663: 1, S0408: 1, H0208: 1, H0619: 1, H0645: 1, H0351: 1, H0411: 1, S0222: 1, H0453: 1, H0392: 1, H0455: 1, H0587: 1, H0632: 1, T0114: 1, H0427: 1, H0156: 1, H0575: 1, S0474: 1, H0309: 1, H0596: 1, H0046: 1, H0083: 1, H0355: 1, S0022: 1, H0615: 1, H0031: 1, H0553: 1, H0628: 1, H0212: 1, H0068: 1, S0036: 1, H0268: 1, H0623: 1, T0069: 1, H0494: 1, S0370: 1, H0633: 1, S0210: 1, L0598: 1, | | | | | | | | |
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| | | | | | | | | | H0529: 1, L0637: 1, L0641: 1, L0764: 1, L0771: 1, L0773: 1, L0662: 1, L0649: 1, L0388: 1, L0774: 1, L0607: 1, L0636: 1, L0783: 1, L0647: 1, L0790: 1, S0374: 1, L0438: 1, H0519: 1, S0126: 1, S0378: 1, H0518: 1, H0696: 1, H0436: 1, S0027: 1, L0744: 1, L0749: 1, L0755: 1, L0759: 1, H0445: 1, L0581: 1, S0011: 1, H0653: 1, S0242: 1, H0422: 1, S0042: 1 and S0424: 1. | | |
| 149 | HODAK55 | 1110333 | 159 | 361 - 2 | 772 | Cys-52 to Trp-58, His-61 to Phe-68. | | AR061: 11, AR089: 9 L0748: 3 and H0328: 1. | | | |
| | | 745532 | 532 | 2 - 169 | 1145 | | | | | | |
| 150 | HSLEI59 | 1128801 | 160 | 770 - 267 | 773 | | | AR089: 1, AR061: 1 S0028: 2, H0171: 1, H0318: 1, S0216: 1, S0044: 1 and S0031: 1 | | | |

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|---|---|
| Thr-29 to Ala-38, Asp-48 to Thr-54, Ala-68 to Glu-78, Ser-101 to Ile-108, Asp-117 to Gln-162, Thr-206 to Trp-212, Cys-285 to Lys-300, Gly-311 to Gly-316, Thr-362 to Thr-367, Arg-376 to Ser-382, Pro-413 to Pro-418, Ser-430 to Gly-435, Asp-484 to Ser-489. | L0777: 11, H0265: 7, L0769: 7, L0747: 5, H0052: 4, L0764: 4, L0438: 4, L0741: 4, L0604: 4, S0358: 3, H0266: 3, H0424: 3, S0344: 3, L0775: 3, L0776: 3, L0758: 3, S0212: 2, H0402: 2, S0007: 2, S0046: 2, S0132: 2, S0222: 2, H0253: 2, S0051: 2, H0594: 2, H0328: 2, H0213: 2, H0617: 2, H0674: 2, H0412: 2, H0100: 2, H0647: 2, S0002: 2, L0761: 2, L0774: 2, L0809: 2, S0152: 2, L0742: 2, L0439: 2, L0755: 2, L0757: 2, H0445: 2, L0594: 2, H0542: 2, H0543: 2, H0484: 1, H0254: 1, H0255: 1, H0125: 1, S0418: 1, S0360: 1, H0580: 1, |
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| 154 | HAGAX57 | 969432 | 536 | 3 - 1448 | 1149 | | | | | Tyr-7 to Tyr-15, Pro-43 to Ala-52, Gln-57 to Ala-62, Asn-68 to Ala-73, Tyr-75 to Met-83, Glu-115 to Leu-140, Ala-144 to Glu-156, Val-159 to Ser-166, Arg-178 to Pro-186, Arg-191 to Ile-198. | AR061: 9, AR089: 4, L0748: 13, L0752: 8, L0438: 4, H0212: 3, S0328: 3, S0010: 2, L0764: 2, L0776: 2, L0659: 2, L0749: 2, L0779: 2, L0599: 2, H0170: 1, T0104: 1, H0331: 1, H0574: 1, H0052: 1, H0596: 1, S0050: 1, H0051: 1, L0483: 1, H0032: 1, H0068: 1, S0466: 1, S0422: 1, L0800: 1, | | |
| | | 1150865 | 164 | 192 - 785 | 777 | | | | | | | | |

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| | | | | | | | | | L0803: 1, L0651: 1, L0791: 1, H0539: 1, H0521: 1, L0780: 1, L0753: 1, L0758: 1 and S0192: 1. | | |
| | 949211 | 537 | 185 - 778 | 1150 | Tyr-7 to Tyr-15, Pro-43 to Ala-52, Gln-57 to Ala-62, Asn-68 to Ala-73, Tyr-75 to Met-83, Glu-115 to Leu-140, Ala-144 to Glu-156, Val-159 to Ser-166, Arg-178 to Pro-186, Arg-191 to Ile-198. | | | | | | |
| 155 | HAMGX15 | 1177932 | 165 | 293 - 763 | 778 | | | | AR089: 4, AR061: 2 H0551: 2, H0581: 1, H0560: 1, H0414: 1, S0152: 1 and H0522: 1. | | |
| | 908840 | 538 | 428 - 757 | 1151 | Ala-54 to Ile-59, His-71 to His-82. | | | | | | |
| 156 | HAUBV06 | 1106041 | 166 | 1164 - 2108 | 779 | Met-5 to Asn-11, Gly-20 to Arg-30, Thr-36 to Ile-41, His-136 to Thr-143, Thr-152 to Asp-161, | | | AR061: 1, AR089: 0 S0052: 2, S0028: 2, H0624: 1, H0294: 1, S0001: 1, S0282: 1, H0250: 1, H0271: 1, | | |

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| 162 | HEOPR74 | 935730 | 545 | 161 - 445 | 1158 | Gln-38 to Ser-51. | AR089: 3, AR061: 2 H0457: 8, H0264: 2, H0645: 1, H0549: 1, H0069: 1, H0599: 1, H0318: 1, H0566: 1, H0132: 1, H0658: 1 and S0350: 1. | | |
| | | 1226822 | 172 | 2 - 937 | 785 | Pro-1 to Gln-8, Lys-32 to Lys-45, Pro-51 to Arg-59, Asp-84 to Val-107, Ala-113 to Leu-135, Gln-137 to Leu-156, Gln-160 to Arg-170, Gln-182 to Pro-194, Lys-201 to Ser-213, Arg-272 to Tyr-278. | | | |
| | | 908836 | 546 | 2 - 649 | 1159 | Pro-1 to Gln-8, Lys-32 to Lys-45, Pro-51 to Arg-59, Asp-84 to Val-107, Ala-113 to Leu-135, Gln-137 to Leu-156, Gln-160 to Arg-170, Gln-182 to Leu-198. | | | |
| 163 | HIBEK35 | 731480 | 173 | 3 - 416 | 786 | | AR089: 0, AR061: 0 T0010: 2 | | |
| 164 | HUMAR88 | 1104937 | 174 | 3 - 551 | 787 | Ala-11 to Asn-16, Ala-18 to Leu-25, Lys-40 to Arg-52, Tyr-58 to Ile-76, Lys-151 to Thr-162, | AR089: 14, AR061: 5 H0545: 1, H0560: 1 and L0805: 1. | | |

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| | | | | | Gln-176 to Gly-182. | | | | |
| | 908839 | 547 | 6 - 344 | 1160 | Ser-111 to Ala-21, Asp-23 to Ile-28. | | | | |
| 165 | HMWGU56 | 1226470 | 175 | 800 - 3 | 788 | | | | AR061: 4, AR089: 3 H0521: 4, H0265: 1, H0341: 1, S0212: 1, S0418: 1, S0356: 1, H0619: 1, T0114: 1, H0004: 1, T0048: 1, H0052: 1, H0081: 1, H0024: 1, H0124: 1, H0040: 1, H0551: 1, H0477: 1, H0623: 1, H0059: 1, H0494: 1, H0641: 1, S0144: 1, S0126: 1, H0660: 1, H0672: 1, L0743: 1 and H0445: 1. |
| | 908825 | 548 | 3 - 776 | 1161 | Met-16 to Ala-23, Ile-34 to Arg-41, Lys-48 to Pro-54, Leu-65 to Thr-82, Glu-104 to Thr-110, Arg-119 to Tyr-126, Gly-135 to Ala-144, His-153 to His-158, | | | | |

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| 166 | HOUDS09 | 1164010 | 176 | 3 - 1121 | 789 | Asn-178 to Gln-194, Arg-197 to His-202, Ser-236 to Arg-241, Gln-245 to Arg-250. | AR061: 153, AR089: 48 L0599: 12, L0766: 11, L0754: 8, L0803: 2, L0809: 2, L0743: 2, L0731: 2, H0624: 1, H0171: 1, S0040: 1, H0650: 1, H0656: 1, S0298: 1, S0282: 1, H0580: 1, S0046: 1, S0222: 1, H0431: 1, H0587: 1, H0486: 1, S0010: 1, H0318: 1, H0581: 1, H0309: 1, H0416: 1, T0006: 1, H0063: 1, T0041: 1, H0560: 1, S0422: 1, S0002: 1, L0641: 1, L0363: 1, L0523: 1, L0659: 1, H0547: 1, H0539: 1, S0152: 1, H0521: 1, L0758: 1, | | |
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| 167 | HTEGM38 | 675087 | 177 | 84 - 263 | 790 | Cys-3 to Glu-8, Gly-13 to Gln-19, Pro-52 to Val-88. | AR089: 1, AR061: 0 H0038: 2 | 11q25 | 602782 |
| 168 | HTEKY82 | 1152495 | 178 | 499 - 125 | 791 | Gln-85 to Gly-91, Ser-99 to Arg-104. | AR061: 5, AR089: 2 H0038: 3, H0575: 1, H0052: 1, H0628: 1, H0412: 1, L0780: 1 and L0758: 1. | | |
| 169 | HTLCY54 | 1193550 | 179 | 1043 - 510 | 792 | | AR061: 5, AR089: 5 H0253: 4, H0618: 3, L0758: 3, L0779: 2 and L0794: 1. | | |
| 170 | HFOXK14 | 603245 | 180 | 150 - 401 | 793 | Arg-1 to Arg-6, Ala-49 to Tyr-58, Pro-67 to Lys-80, Ser-92 to Trp-108. Ala-6 to Tyr-17. | AR089: 19, AR061: 8 L0747: 5, L0731: 2, H0656: 1, H0351: 1, H0392: 1, H0333: 1, S0362: 1, S0306: 1, | | |

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| | | | | | | | | S0002: 1, L0770: 1, L0648: 1, L0776: 1, H0547: 1, H0555: 1 and S0276: 1. | | | |
| 171 | HHFFO69 | 837703 | 181 | 1 - 723 | 794 | | | AR089: 1, AR061: 1 S0005: 1, H0457: 1, H0009: 1, H0050: 1, S6028: 1, S0036: 1 and H0135: 1. | | | |
| 172 | HHFLU06 | 857884 | 182 | 2 - 328 | 795 | | | AR061: 5, AR089: 2 H0619: 1 | | | |
| 173 | HAGBA56 | 732597 | 183 | 115 - 633 | 796 | Asp-52 to Leu-57, Lys-82 to Thr-87, Ser-90 to Trp-98, Ser-118 to Leu-123. | | AR061: 2, AR089: 1 S0010: 1, H0135: 1, L0766: 1, L0745: 1, L0779: 1 and L0758: 1. | 7q21-q22 | 116860, 126650, 126650, 129900, 133170, 154276, 173360, 173360, 602136, 602136, 602136, 602447 | |
| 174 | HAGGF84 | 911312 | 184 | 1 - 333 | 797 | Lys-14 to Glu-27. | | AR061: 3, AR089: 2 L0766: 18, L0748: 11, L0439: 9, L0749: 8, | | | |

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| | | L0438: 5, L0750: 5, L0777: 4, L0759: 4, H0441: 3, H0052: 3, L0637: 3, L0761: 3, L0740: 3, L0747: 3, L0103: 2, H0574: 2, H0156: 2, H0597: 2, S0250: 2, L0649: 2, L0803: 2, L0806: 2, L0792: 2, S3014: 2, L0757: 2, L0485: 2, L0599: 2, H0171: 1, S6024: 1, L0002: 1, H0657: 1, H0341: 1, S0358: 1, S0360: 1, S0132: 1, L0717: 1, H0632: 1, H0013: 1, H0599: 1, S0010: 1, S0346: 1, H0318: 1, H0251: 1, T0115: 1, H0544: 1, L0471: 1, H0014: 1, S0362: 1, H0083: 1, H0188: 1, H0428: 1, H0646: 1, H0538: 1, L0598: 1, L0762: 1, L0763: 1, | | | | | |
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| 175 | HAHGD33 | 921782 | 185 | 1 - 1020 | 798 | Phe-22 to Ala-37, Cys-94 to Asn-100, Gly-137 to Pro-145, Glu-172 to Ala-179, Ile-217 to Asp-222. | AR061: 7, AR089: 5 H0039: 5, H0622: 5, L0748: 4, H0667: 4, H0255: 3, S0126: 3, H0393: 2, S0278: 2, H0599: 2, H0618: 2, H0318: 2, H0123: 2, H0050: 2, H0179: 2, H0271: 2, S0036: 2, H0135: 2, H0634: 2, H0087: 2, H0100: 2, H0633: 2, S0210: 2, | AR061: 7, AR089: 5 H0039: 5, H0622: 5, L0748: 4, H0667: 4, H0255: 3, S0126: 3, H0393: 2, S0278: 2, H0599: 2, H0618: 2, H0318: 2, H0123: 2, H0050: 2, H0179: 2, H0271: 2, S0036: 2, H0135: 2, H0634: 2, H0087: 2, H0100: 2, H0633: 2, S0210: 2, | 19p | L0769: 1, L0662: 1, L0768: 1, L0776: 1, L0655: 1, L0659: 1, L0526: 1, L0783: 1, L0789: 1, L0665: 1, S0148: 1, H0520: 1, H0519: 1, S0330: 1, L0602: 1, S0152: 1, S0136: 1, S0350: 1, L0752: 1, H0343: 1, L0366: 1, S0011: 1, H0665: 1, S0196: 1, H0423: 1, L0697: 1 and S0462: 1. | | |
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| | | | | | S0002: 2, H0144: 2, L0438: 2, L0602: 2, L0744: 2, L0731: 2, L0595: 2, L0601: 2, H0665: 2, H0542: 2, H0556: 1, H0222: 1, H0294: 1, H0583: 1, H0650: 1, H0657: 1, H0484: 1, H0306: 1, S0418: 1, S0420: 1, S0354: 1, H0580: 1, S0007: 1, S0046: 1, H0619: 1, H0550: 1, H0392: 1, H0586: 1, H0333: 1, H0486: 1, H0122: 1, H0196: 1, H0597: 1, H0544: 1, H0009: 1, H0172: 1, L0471: 1, H0023: 1, H0071: 1, H0266: 1, H0290: 1, H0553: 1, H0628: 1, H0551: 1, H0056: 1, H0623: 1, S0038: 1, H0494: 1, H0625: 1, H0561: 1, H0386: 1, H0509: 1, | | | | |
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| 176 | HAHY08 | 962113 | 186 | 3 - 278 | 799 | | | | AR061: 10, AR089: 6 | | | |
| 177 | HBIOZ10 | 973131 | 187 | 3 - 503 | 800 | | | Leu-50 to Asp-61, Ser-100 to Leu-107, Ala-120 to Thr-130. | AR054: 189, AR051: 68, AR050: 35, AR089: 4, AR061: 3 H0593: 1 | | | |
| 178 | HBKDI30 | 729048 | 188 | 1 - 381 | 801 | | | Gly-15 to Thr-21, Glu-76 to Lys-86. | AR089: 1, AR061: 0 S0364: 3, S0366: 3, L0604: 3, H0624: 1, L0622: 1, L0623: 1, H0041: 1, L0791: 1, S0380: 1 and L0748: 1. | | | |

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| 179 | HBXBW40 | 706115 | 189 | 124 - 456 | 802 | Gln-3 to Ser-12, Arg-33 to Arg-50, Ser-93 to Glu-98. | AR089: 16, AR061: 8 S0038: 2, H0438: 1, S0049: 1 and H0547: 1. | | |
| 180 | HCEHE35 | 909937 | 190 | 3 - 392 | 803 | Asn-6 to Pro-13. | AR061: 8, AR089: 3 S0222: 1, H0052: 1, H0194: 1, H0290: 1 and H0264: 1. | | |
| 181 | HCEPW85 | 911374 | 191 | 3 - 314 | 804 | Thr-2 to Gln-7. | H0052: 1 and L0471: 1. | | |
| 182 | HCFAT25 | 932068 | 192 | 82 - 588 | 805 | Lys-15 to Ser-20, Arg-51 to Arg-60, Lys-64 to Pro-101. | AR061: 2, AR089: 2 S0358: 1, H0413: 1, L0502: 1, L0657: 1, H0522: 1 and H0422: 1. | | |
| 183 | HCFCF47 | 1139731 | 193 | 3 - 764 | 806 | Leu-1 to Glu-9, Gln-43 to Ala-52, Gly-169 to Gly-176, Arg-178 to Leu-185, Pro-192 to Phe-199. | AR089: 14, AR061: 7 H0341: 1 and H0422: 1. | | |
| | | 894415 | 552 | 2 - 298 | 1165 | Arg-1 to Glu-8. | | | |
| 184 | HDAAV61 | 810305 | 194 | 2 - 343 | 807 | Asp-90 to Lys-105. | AR089: 25, AR061: 11 5q34 L0601: 5, H0266: 4, S0222: 3, H0265: 2, H0556: 2, H0575: 2, H0052: 2, H0271: 2, S0114: 1, S0134: 1, S0420: 1, H0393: 1, | 109690, 109690, 123101, 180071, 600584 | |

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| | | | | | | | | | H0550: 1, H0497: 1, H0318: 1, H0581: 1, H0251: 1, T0115: 1, H0014: 1, H0286: 1, H0494: 1, H0561: 1, L0766: 1, L0657: 1, H0698: 1, H0684: 1, S0330: 1, H0521: 1, S3014: 1, L0777: 1, S0260: 1, L0591: 1, L0594: 1 and H0543: 1. | | | |
| 185 | HDPKD75 | 810824 | 195 | 2 - 445 | 808 | Ala-13 to Asn-20, Phe-38 to Gly-46, Glu-89 to His-95. | | | AR089: 4, AR061: 0 H0581: 1, H0494: 1, H0521: 1, H0543: 1 and L0465: 1. | | | |
| 186 | HDPNC96 | 934520 | 196 | 3 - 734 | 809 | Val-2 to Gly-8, Asp-20 to Gln-26. | | | AR089: 1, AR061: 1 H0522: 2 and L0766: 1. | | | |
| 187 | HDPSR15 | 969666 | 197 | 168 - 785 | 810 | Pro-26 to Leu-34, His-42 to Asn-51. | | | AR061: 2, AR089: 2 L0759: 12, L0439: 11, L0766: 7, L0775: 5, H0521: 5, L0755: 5, L0748: 4, L0756: 4, L0777: 4, L0731: 4, L0581: 4, L0619: 3, L0666: 3, L0779: 3, | 9 | | |

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| 188 | HDQDX20 | 919027 | 198 | 210 - 1037 | 811 | Met-7 to Ser-12, Ser-20 to Arg-30, Asp-85 to Ala-92, Met-119 to Asn-146, Pro-151 to Asp-161. | L0749: 1, L0603: 1, H0665: 1 and H0542: 1. | | |
| 189 | HDQHB19 | 1226089 | 199 | 1 - 747 | 812 | Phe-73 to Pro-81, His-156 to Asp-165, Pro-182 to Lys-187, Lys-196 to Asp-201, Pro-204 to Leu-214, Pro-224 to Asp-231. | AR089: 30, AR061: 4 H0521: 3, H0051: 2, L0756: 2, H0590: 1, S0250: 1, L0772: 1, H0522: 1, S0406: 1 and L0748: 1. | | |
| | | | | | | | AR061: 3, AR089: 3 L0759: 12, L0439: 11, L0766: 7, L0775: 5, H0521: 5, L0755: 5, L0748: 4, L0756: 4, L0777: 4, L0731: 4, L0581: 4, L0619: 3, L0666: 3, L0779: 3, L0757: 3, L0588: 3, S0418: 2, L0618: 2, H0580: 2, L0055: 2, L0769: 2, L0773: 2, L0774: 2, L0791: 2, L0747: 2, L0750: 2, H0265: 1, H0663: 1, S0356: 1, H0208: 1, H0370: 1, H0108: 1, H0575: 1, H0618: 1, | | |

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| | | | | | | | | | H0544: 1, H0545: 1, S0050: 1, H0510: 1, H0286: 1, H0031: 1, H0644: 1, H0068: 1, H0135: 1, L0564: 1, H0494: 1, L0475: 1, H0396: 1, S0144: 1, S0002: 1, S0426: 1, L0763: 1, L0761: 1, L0642: 1, L0764: 1, L0662: 1, L0768: 1, L0806: 1, L0661: 1, L0659: 1, L0367: 1, L0663: 1, H0519: 1, H0435: 1, H0658: 1, S3014: 1, L0751: 1, L0749: 1, L0603: 1, H0665: 1 and H0542: 1. | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
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| 192 | HE8UY74 | 960914 | 202 | 111 - 455 | 815 | | AR061: 2, AR089: 1 H0013: 1 and S0027: 1. | | |
| 193 | HE9NO66 | 974353 | 203 | 362 - 871 | 816 | Phe-8 to Lys-27, Ser-79 to Ser-87, Cys-102 to Val-116. | AR061: 1, AR089: 1 L0774: 2 and H0144: 2. | | |
| 194 | HEMBT61 | 939957 | 204 | 1 - 351 | 817 | | AR061: 8, AR089: 4 L0547: 2, S0046: 1, L0471: 1, L0772: 1, L0529: 1 and L0780: 1. | | |
| 195 | HETLF29 | 909762 | 205 | 3 - 416 | 818 | | AR061: 4, AR089: 2 H0046: 1 and L0758: 1. | | |
| 196 | HFIUE75 | 909758 | 206 | 2 - 775 | 819 | Cys-1 to Val-10, Ala-14 to Met-22. | AR089: 1, AR061: 1 L0748: 5, S0242: 3, H0615: 2, S0376: 1, S0360: 1, L0717: 1, L0641: 1, L0766: 1, L0664: 1, H0478: 1, L0593: 1 and S0196: 1. | | |
| 197 | HFKIT06 | 934019 | 207 | 1 - 300 | 820 | Asp-2 to Pro-7, Pro-15 to Gln-20. | AR089: 0, AR061: 0 H0620: 2, L0761: 2, L0766: 2, L0744: 2, L0754: 2, L0596: 2, H0686: 1, H0295: 1, H0657: 1, H0597: 1, H0009: 1, H0264: 1. | | |

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| | | | | | | | | S0002: 1, L0769: 1, L0774: 1, L0805: 1, L0657: 1, L0790: 1, H0690: 1 and H0521: 1. | | | |
| 198 | HHEGG20 | 894409 | 208 | 26 - 820 | 821 | | | AR089: 2, AR061: 1 S0360: 1, H0013: 1, L0664: 1 and H0542: 1. | | | |
| 199 | HHEHC53 | 921783 | 209 | 3 - 908 | 822 | Gly-59 to Ser-68, Ala-87 to Glu-98, Pro-106 to Asn-121, Ser-148 to Lys-159, Phe-207 to Ala-222, Ile-284 to Lys-289. | | AR089: 3, AR061: 2 L0748: 8, H0039: 5, H0622: 5, L0664: 5, L0439: 5, L0779: 5, L0731: 5, L0758: 5, L0665: 4, L0744: 4, L0601: 4, H0667: 4, H0255: 3, H0618: 3, L0666: 3, L0438: 3, S0126: 3, L0602: 3, L0742: 3, L0604: 3, L0595: 3, H0542: 3, H0265: 2, S0358: 2, H0393: 2, S0278: 2, H0550: 2, H0333: 2, H0599: 2, H0318: 2, H0545: 2, H0123: 2, H0050: 2, H0620: 2, H0179: 2, H0271: 2, | 19p | | |

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| | | | | S0036: 2, H0135: 2, H0634: 2, H0087: 2, H0100: 2, H0633: 2, S0210: 2, S0002: 2, L0769: 2, L0646: 2, L0768: 2, L0774: 2, H0144: 2, L0565: 2, H0689: 2, S0027: 2, L0747: 2, L0755: 2, L0593: 2, H0665: 2, H0556: 1, T0002: 1, H0222: 1, H0685: 1, H0294: 1, S0430: 1, H0583: 1, H0650: 1, H0657: 1, S0212: 1, S0282: 1, H0484: 1, H0306: 1, S0418: 1, S0420: 1, S0354: 1, S0360: 1, H0580: 1, S0007: 1, S0046: 1, H0619: 1, H0351: 1, H0549: 1, H0392: 1, H0586: 1, H0486: 1, T0060: 1, L0022: 1, H0122: 1, H0196: 1, H0597: 1, H0544: 1. | | | | |
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| | | | | | H0009: 1, H0172: 1, L0471: 1, H0023: 1, H0071: 1, H0266: 1, H0290: 1, S0022: 1, H0030: 1, H0553: 1, H0628: 1, H0182: 1, H0617: 1, H0606: 1, H0551: 1, H0413: 1, H0056: 1, H0623: 1, S0038: 1, H0494: 1, H0625: 1, H0561: 1, H0386: 1, H0509: 1, H0131: 1, H0130: 1, H0646: 1, S0144: 1, S0344: 1, S0426: 1, H0529: 1, L0763: 1, L0770: 1, L0637: 1, L0372: 1, L0662: 1, L0775: 1, L0776: 1, L0659: 1, L0383: 1, L0790: 1, H0547: 1, H0435: 1, H0658: 1, H0670: 1, S0330: 1, H0521: 1, H0436: 1, S0390: 1, S0028: 1, S0032: 1, L0750: 1, | | | | |
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| | | | | | | | | | L0753: 1, L0757: 1, L0759: 1, S0260: 1, H0445: 1, H0595: 1, L0597: 1, L0366: 1, H0668: 1, S0242: 1, H0423: 1, H0422: 1 and H0352: 1. | | |
| 200 | HHERQ79 | 944057 | 210 | 88 - 474 | 823 | Ser-3 to Thr-11, Lys-32 to Gly-39, Thr-50 to Glu-57, Thr-83 to Gln-88. | | | AR089: 3, AR061: 2 H0597: 1, H0435: 1 and H0543: 1. | | |
| 201 | HISAF59 | 959140 | 211 | 130 - 843 | 824 | Gly-33 to Ser-48. | | | AR089: 2, AR061: 2 L0789: 4, L0758: 4, H0657: 3, H0052: 3, H0046: 3, L0438: 3, L0744: 3, L0779: 3, L0005: 2, H0586: 2, H0581: 2, H0194: 2, H0038: 2, L0800: 2, L0659: 2, H0521: 2, L0743: 2, L0439: 2, H0556: 1, S0282: 1, S0358: 1, H0619: 1, H0618: 1, H0231: 1, H0569: 1, S0362: 1, H0622: 1, T0006: 1, | | |

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| 202 | HKAKMI0 | 918685 | 212 | 2 - 547 | 825 | Gly-25 to Gln-31, Asn-58 to Leu-63, Lys-71 to His-76, Ile-82 to Arg-88, Ala-134 to Thr-139. | <p>H0135: 1, H0616: 1, H0413: 1, H0623: 1, L0351: 1, S0150: 1, L0769: 1, L0372: 1, L0662: 1, L0794: 1, L0775: 1, L0651: 1, L0527: 1, L0657: 1, L0666: 1, H0144: 1, H0547: 1, H0690: 1, H0658: 1, H0672: 1, H0539: 1, S0378: 1, H0555: 1, L0754: 1, L0747: 1, L0780: 1, L0596: 1, S0192: 1, H0542: 1 and H0423: 1.</p> <p>AR089: 1, AR061: 1 L0794: 4, L0438: 4, L0761: 3, L0766: 3, L0748: 3, L0439: 3, H0556: 2, L0602: 2, L0754: 2, L0779: 2, H0580: 1, H0208: 1, H0013: 1, T0082: 1, S0010: 1, H0428: 1, H0553: 1, H0038: 1, H0616: 1, H0494: 1,</p> | | |
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| | | | | | | | | | L0796: 1, L0800: 1, L0773: 1, L0533: 1, L0803: 1, L0776: 1, L0657: 1, L0791: 1, H0520: 1, H0519: 1, H0521: 1, H0187: 1, L0731: 1, S0031: 1 and L0366: 1. | | | |
| 203 | HLTHP86 | 919354 | 213 | 3 - 1310 | 826 | | | | AR089: 1, AR061: 1 L0439: 3, L0438: 2, S0028: 2, H0656: 1, H0645: 1, H0369: 1, S0222: 1, S0346: 1, H0328: 1, H0029: 1, H0644: 1, H0169: 1, H0591: 1, H0646: 1, H0520: 1, H0539: 1, L0746: 1 and L0366: 1. | | | |
| 204 | HMSJL96 | 934483 | 214 | 1 - 426 | 827 | Thr-15 to Arg-22, Ala-38 to Met-43, Gln-49 to Lys-64, Thr-97 to Gln-108, Thr-131 to Lys-137. | | | AR054: 16, AR051: 15, AR050: 12, AR089: 0, AR061: 0 L0777: 6, L0758: 5, L0779: 4, L0803: 3, S0358: 2, H0004: 2, L0662: 2, L0775: 2, H0144: 2, S0126: 2, | | | |

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| | | | | | S0328: 2, S3014: 2, S0027: 2, L0743: 2, L0748: 2, H0265: 1, H0656: 1, S0212: 1, H0663: 1, H0638: 1, H0580: 1, H0632: 1, H0486: 1, H0599: 1, H0618: 1, L0105: 1, H0251: 1, H0309: 1, H0544: 1, H0123: 1, H0050: 1, L0471: 1, H0024: 1, H0399: 1, S0003: 1, H0364: 1, H0553: 1, H0038: 1, H0412: 1, H0413: 1, T0041: 1, S0344: 1, S0002: 1, L0598: 1, H0529: 1, L0645: 1, L0363: 1, L0649: 1, L0804: 1, L0805: 1, L0558: 1, L0659: 1, L0528: 1, L0789: 1, L0792: 1, L0666: 1, S0374: 1, H0555: 1, S3012: 1, S0028: 1, S0206: 1, S0032: 1, |
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| 205 | HMTAJ73 | 813296 | 215 | 1 - 438 | 828 | Pro-23 to Lys-28, Gln-39 to Thr-51, Lys-93 to Ala-106, Gln-112 to Pro-129, Pro-132 to Pro-143. | L0439: 1, L0757: 1, S0031: 1, H0707: 1, S0192: 1, H0423: 1, S0042: 1 and H0008: 1. AR061: 24, AR089: 14 L0806: 3, L0772: 2, L0648: 2, H0255: 1, L0717: 1, H0586: 1, H0599: 1, H0618: 1, H0581: 1, H0052: 1, H0123: 1, L0629: 1, L0659: 1, L0663: 1, S0330: 1, H0518: 1 and H0555: 1. | | | |
| 206 | HNTCP13 | 909770 | 216 | 1 - 960 | 829 | | AR061: 3, AR089: 2 L0750: 4, H0519: 3, L0666: 2, L0565: 2, H0539: 2, L0742: 2, L0744: 2, L0754: 2, L0777: 2, L0759: 2, H0662: 1, S0045: 1, S0346: 1, H0251: 1, H0030: 1, H0628: 1, H0674: 1, H0529: 1, L0770: 1, L0764: 1, L0526: 1, L0783: 1. | 12q12-q13.1 | 126337, 600194, 600231, 600808, 601284, 601769, 601769, 602116 | |

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| | | | | | | | | | L0787: 1, H0547: 1, H0521: 1, H0696: 1, H0555: 1, L0747: 1, L0749: 1, L0786: 1, L0779: 1, L0780: 1, L0752: 1 and L0592: 1. | | | |
| 207 | HNTMD79 | 934522 | 217 | 182 - 586 | 830 | | | | AR089: 2, AR061: 2 H0519: 2, S0420: 1, T0114: 1, H0013: 1, S0346: 1, H0038: 1, S0142: 1, H0520: 1, H0521: 1 and H0136: 1. | | | |
| 208 | HNTMH70 | 757184 | 218 | 2 - 688 | 831 | Pro-1 to Glu-6, His-17 to Lys-22, Pro-52 to Gln-58. | | | AR089: 0, AR061: 0 H0520: 1 | | | |
| 209 | HNTNB14 | 909942 | 219 | 2 - 658 | 832 | Ala-2 to Gln-9, Arg-22 to Val-29, Glu-51 to Leu-64. | | | AR089: 1, AR061: 1 S0007: 1, S0222: 1, S0049: 1, L0438: 1, H0520: 1 and L0439: 1. | | | |
| 210 | HODFF88 | 974911 | 220 | 14 - 544 | 833 | His-8 to Gly-18, Glu-150 to Leu-167. | | | AR054: 34, AR051: 29, AR050: 23, AR089: 4, AR061: 4 H0615: 1 | | | |
| 211 | HOHCE47 | 1216683 | 221 | 629 - 2161 | 834 | Tyr-83 to Ser-92, Leu-118 to Tyr-123, Leu-137 to Ser-143, | | | AR061: 1, AR089: 0 S0040: 1, H0580: 1, S0222: 1, H0355: 1, | | | |

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| | | | | | | Gln-148 to Ser-158. | S0250: 1, L0565: 1 and S0152: 1. | | |
| 212 | HPCRV84 | 911566 | 554 | 1 - 429 | 1167 | Gly-1 to Trp-6. | | | |
| | | 945856 | 222 | 112 - 417 | 835 | Thr-1 to Leu-12. | AR089: 0, AR061: 0 | | |
| 213 | HRACK83 | 888037 | 223 | 1 - 471 | 836 | Gln-15 to Gln-21. | AR089: 3, AR061: 2 L0803: 4, L0758: 3, S0212: 2, S0358: 2, H0038: 2, L0770: 2, L0767: 2, L0766: 2, L0748: 2, L0751: 2, L0747: 2, L0759: 2, L0588: 2, L0599: 2, H0411: 1, H0392: 1, H0333: 1, L0021: 1, H0118: 1, T0115: 1, L0471: 1, L0163: 1, H0633: 1, L0769: 1, L0764: 1, L0775: 1, L0376: 1, L0806: 1, L0805: 1, L0807: 1, L0787: 1, H0547: 1, S0122: 1, H0555: 1, H0478: 1, L0744: 1, L0740: 1, L0749: 1, L0750: 1, L0755: 1 and | | |

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| 214 | HRADM45 | 717358 | 224 | 2 - 472 | 837 | Lys-1 to Leu-6, Asp-25 to Pro-30. | L0595: 1. AR089: 14, AR061: 6 H0555: 1 and L0777: 1. | | |
| 215 | HRAED74 | 942527 | 225 | 289 - 651 | 838 | His-9 to Ile-15. | AR061: 1, AR089: 1 S0222: 3, H0052: 3, L0361: 3, H0179: 2, L0769: 2, H0521: 2, H0555: 2, L0779: 2, L0758: 2, H0663: 1, H0549: 1, S0220: 1, H0586: 1, H0156: 1, S0010: 1, H0596: 1, S0051: 1, T0010: 1, H0271: 1, L0143: 1, H0617: 1, H0652: 1, L0764: 1, L0794: 1, L0806: 1, L0809: 1, H0518: 1, H0478: 1, L0751: 1, L0747: 1, L0750: 1, L0780: 1, L0731: 1 and L0366: 1. | | |
| 216 | HRDZ70 | 942673 | 226 | 3 - 440 | 839 | Lys-49 to Lys-54, Trp-106 to Lys-112, Leu-130 to Gly-141. | AR089: 12, AR061: 4 H0598: 1 and H0135: 1. | | |
| 217 | HSKAC24 | 823869 | 227 | 98 - 481 | 840 | Ser-1 to Asp-7, | AR061: 2, AR089: 1 | | |

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| 218 | HSSMT34 | 911294 | 228 | 56 - 553 | 841 | Leu-38 to Ser-44, Pro-85 to Tyr-90. Glu-29 to Arg-35, Arg-50 to Leu-55, Leu-60 to Ser-69, Lys-102 to Asp-108, Pro-133 to Gln-141. | H0370: 2, S0002: 1, S0428: 1 and S0027: 1. AR061: 4, AR089: 3 L0439: 6, L0777: 6, H0052: 4, L0748: 4, H0634: 3, L0662: 3, L0805: 3, L0659: 3, L0438: 3, H0547: 3, L0750: 3, L0758: 3, H0208: 2, H0123: 2, H0014: 2, H0617: 2, H0135: 2, L0769: 2, L0766: 2, L0803: 2, L0776: 2, L0666: 2, L0751: 2, L0745: 2, L0731: 2, H0265: 1, S0408: 1, H0549: 1, H0497: 1, L0622: 1, H0581: 1, H0194: 1, L0738: 1, H0546: 1, H0024: 1, S0362: 1, L0163: 1, T0010: 1, H0083: 1, H0510: 1, H0266: 1, H0428: 1, H0622: 1, H0673: 1, H0598: 1, S0036: 1, | | |
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| 222 | HTEMU66 | 944419 | 232 | 454 - 963 | 845 | Ala-1 to Gln-7, Lys-24 to Ser-30, Pro-44 to Asn-53, Glu-104 to Asp-112, Leu-152 to Ser-157. | AR061: 7, AR089: 5 H0616: 1 | L0752: 3, S0360: 2, L0748: 2, L0746: 2, L0755: 2, H0624: 1, S0114: 1, H0098: 1, L0471: 1, H0083: 1, H0428: 1, L0483: 1, H0090: 1, H0616: 1, H0494: 1, H0560: 1, H0509: 1, L0761: 1, L0772: 1, L0803: 1, L0776: 1, L0655: 1, L0792: 1, L0664: 1, S0374: 1, L0438: 1, H0520: 1, H0519: 1, H0435: 1, H0648: 1, S0152: 1, H0521: 1, H0478: 1, L0747: 1, L0756: 1, L0779: 1, L0758: 1, L0759: 1, H0667: 1, H0543: 1 and L0465: 1. | | |
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| 223 | HTEMV09 | 909843 | 233 | 1 - 711 | 846 | Asp-22 to Asp-28, Leu-98 to Trp-103, Glu-123 to Trp-154. | AR089: 13, AR061: 13 L0666: 3, L0758: 3, H0616: 2, L0779: 2, S0036: 1, L0598: 1, L0766: 1, L0651: 1, L0806: 1, L0776: 1, H0144: 1, H0547: 1, H0672: 1 and H0555: 1. | | |
| 224 | HTEMV66 | 1151075 | 234 | 861 - 175 | 847 | Ile-39 to Ser-46, Val-69 to Gln-75, Phe-90 to Ser-100. | AR061: 5, AR089: 1 H0616: 1 and L0758: 1. | | |
| | | 813038 | 555 | 1 - 318 | 1168 | Ser-38 to Pro-45. | | | |
| 225 | HTGAU79 | 1175071 | 235 | 62 - 976 | 848 | His-12 to Arg-20, Pro-26 to Asp-43, Ala-62 to Glu-70, Arg-78 to Arg-83, Phe-100 to Gln-105, Gly-129 to Glu-136, Met-182 to Gly-190, Tyr-277 to Ala-284. | AR061: 7, AR089: 4 H0551: 3, H0529: 3, L0769: 3, L0758: 3, S0418: 2, L0770: 2, L0773: 2, L0521: 2, H0701: 2, S0126: 2, L0747: 2, L0731: 2, L0759: 2, L0589: 2, L0601: 2, H0624: 1, H0149: 1, H0556: 1, H0295: 1, S0134: 1, H0583: 1, H0661: 1, H0592: 1, H0013: 1, H0635: 1, H0581: 1, | | |

Table 3

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| | | | | | | | | | S0250: 1, H0212: 1, H0412: 1, S0144: 1, L0763: 1, L0645: 1, L0764: 1, L0794: 1, L0766: 1, L0775: 1, L0783: 1, L0665: 1, H0519: 1, H0435: 1, H0672: 1, H0436: 1, S3014: 1, S0028: 1, L0750: 1, L0777: 1, L0366: 1, H0667: 1 and H0423: 1. | | |
| 226 | HTLEJ11 | 940369 | 556 | 63 - 977 | 1169 | His-12 to Arg-20, Pro-26 to Asp-43, Ala-62 to Glu-70, Arg-78 to Arg-83, Phe-100 to Gln-105, Gly-129 to Glu-136. | | | AR061: 3, AR089: 1 H0618: 3 and H0253: 1. | 15q13-qter | |
| 227 | HTLIY52 | 1218691 | 237 | 180 - 1376 | 850 | Tyr-52 to Gln-60, Phe-86 to Ala-94, Lys-111 to Arg-118, His-193 to Tyr-198. Pro-3 to Gly-8, Val-21 to Gly-30, Gly-68 to Ala-85, His-94 to Gly-99, | | | AR061: 0, AR089: 0 H0618: 64, H0253: 52, L0758: 6, L0779: 2, H0392: 1, H0038: 1, | | |

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| | | | | | | | Ala-105 to Arg-110, Ala-114 to Gln-138, Arg-143 to Glu-155, Leu-202 to Arg-222, Arg-287 to Ser-292, Pro-325 to Arg-332, Arg-337 to Gly-351, Pro-389 to Arg-399. | L0761: 1, L0803: 1, L0806: 1 and L0697: 1. | | |
| | | 942161 | 557 | 1 - 1368 | 1170 | | | | | |
| 228 | HTOAK34 | 966800 | 238 | 918 - 1196 | 851 | | Ser-67 to Trp-77. | AR089: 1, AR061: 1 L0766: 2, H0264: 1 and H0521: 1. | | |
| 229 | HTPGG25 | 911282 | 239 | 3 - 392 | 852 | | Pro-3 to Arg-8. | AR061: 2, AR089: 2 L0439: 6, L0777: 6, H0052: 4, L0748: 4, H0634: 3, L0662: 3, L0805: 3, L0659: 3, L0438: 3, H0547: 3, L0750: 3, L0758: 3, H0208: 2, H0123: 2, H0014: 2, H0617: 2, H0135: 2, L0769: 2, L0766: 2, L0803: 2, L0776: 2, L0666: 2, L0751: 2, L0745: 2, L0731: 2, H0265: 1, | | |

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| | S0408: 1, H0549: 1, H0497: 1, L0622: 1, H0581: 1, H0194: 1, L0738: 1, H0546: 1, H0024: 1, S0362: 1, L0163: 1, T0010: 1, H0083: 1, H0510: 1, H0266: 1, H0428: 1, H0622: 1, H0673: 1, H0598: 1, S0036: 1, H0163: 1, H0413: 1, L0370: 1, T0041: 1, H0647: 1, L0637: 1, L0667: 1, L0772: 1, L0646: 1, L0800: 1, L0764: 1, L0649: 1, L0657: 1, L0809: 1, L0788: 1, L0663: 1, S0374: 1, H0520: 1, H0670: 1, H0666: 1, S0330: 1, H0539: 1, H0521: 1, H0696: 1, H0478: 1, S0028: 1, L0741: 1, L0747: 1, L0749: 1, L0780: 1, L0752: 1 and H0543: 1. | | | | | |
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| 230 | HUJAD24 | 1161319 | 240 | 770 - 1237 | 853 | Gln-49 to Thr-69, His-129 to Cys-143. | AR089: 1, AR061: 0 L0750: 3, H0650: 2, H0637: 2, H0265: 1, H0556: 1, S0222: 1, H0040: 1, H0280: 1, L0655: 1, L0789: 1 and L0666: 1. | | |
| | | 911498 | 558 | 3 - 293 | 1171 | | | | |
| 231 | HUTSF11 | 966029 | 241 | 3 - 302 | 854 | Glu-1 to Glu-6, Asn-16 to Arg-22. | AR089: 0, AR061: 0 S0464: 1 and L0356: 1. | | |
| 232 | HUVGZ88 | 1227628 | 242 | 83 - 862 | 855 | Gln-216 to Asp-226, Thr-250 to Thr-256. | AR089: 2, AR061: 2 L0789: 4, L0758: 4, H0657: 3, H0052: 3, L0438: 3, L0744: 3, L0779: 3, L0005: 2, H0581: 2, H0194: 2, H0046: 2, H0038: 2, L0800: 2, L0659: 2, H0521: 2, L0743: 2, L0439: 2, H0556: 1, S0282: 1, S0358: 1, H0619: 1, H0586: 1, H0618: 1, H0231: 1, S0362: 1, H0622: 1, T0006: 1, H0616: 1, H0413: 1, H0623: 1, | | |

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| | | | | | | | | | L0351: 1, S0150: 1, L0769: 1, L0372: 1, L0662: 1, L0794: 1, L0775: 1, L0651: 1, L0527: 1, L0657: 1, L0666: 1, H0547: 1, H0690: 1, H0658: 1, H0672: 1, H0539: 1, S0378: 1, H0555: 1, L0754: 1, L0747: 1, L0780: 1, L0596: 1, S0192: 1, H0542: 1 and H0423: 1. | | |
| 233 | HWADY66 | 959020 | 559 | 83 - 439 | 1172 | Asn-89 to Asn-95. | | | AR061: 1, AR089: 1 H0581: 1, H0494: 1, H0521: 1, H0444: 1, H0543: 1 and L0465: 1. | | |
| | | 1096252 | 243 | 365 - 117 | 856 | | | | | | |
| | | 734565 | 560 | 1 - 186 | 1173 | | | | | | |
| 234 | HWAFG04 | 952878 | 244 | 1658 - 789 | 857 | Gln-110 to Asp-120, Ser-189 to Phe-207, Cys-218 to Ser-228, Gln-240 to Ala-245, Glu-263 to Ser-271. | | | AR089: 17, AR061: 8 L0789: 4, L0758: 4, H0657: 3, H0052: 3, L0438: 3, L0744: 3, L0779: 3, L0005: 2, H0581: 2, H0194: 2, H0046: 2, H0038: 2, | | |

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| 235 | HWAFS18 | 948434 | 245 | 54 - 791 | 858 | Pro-1 to Pro-7, Leu-10 to Lys-18, Val-119 to Lys-126, Gln-146 to Trp-151, | L0800: 2, L0659: 2, H0521: 2, L0743: 2, L0439: 2, H0556: 1, S0282: 1, S0358: 1, H0619: 1, H0586: 1, H0618: 1, H0231: 1, S0362: 1, H0622: 1, T0006: 1, H0616: 1, H0413: 1, H0623: 1, L0351: 1, S0150: 1, L0769: 1, L0372: 1, L0662: 1, L0794: 1, L0775: 1, L0651: 1, L0527: 1, L0657: 1, L0666: 1, H0547: 1, H0690: 1, H0658: 1, H0672: 1, H0539: 1, S0378: 1, H0555: 1, L0754: 1, L0747: 1, L0780: 1, L0596: 1, S0192: 1, H0542: 1 and H0423: 1. | | |
| | | | | | | AR089: 4, AR061: 3 H0581: 3, H0622: 3, H0575: 2, H0090: 2, L0777: 2, L0757: 2, | | | |

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| 236 | HWAGS73 | 1150212 | 246 | 1 - 339 | 859 | Val-14 to Lys-21, Gln-41 to Trp-46, Ala-98 to Pro-103. | S0114: 1, H0650: 1, H0255: 1, S0360: 1, S0278: 1, H0486: 1, H0318: 1, H0457: 1, H0039: 1, H0553: 1, L0763: 1, L0761: 1, L0764: 1, L0789: 1, H0144: 1, S0374: 1, S0310: 1, H0555: 1, L0758: 1, H0445: 1 and S0276: 1. | | |
| | | | | | | | AR089: 2, AR061: 2 H0581: 3, H0622: 3, H0575: 2, H0090: 2, L0777: 2, L0757: 2, S0114: 1, H0650: 1, H0255: 1, S0360: 1, S0278: 1, H0486: 1, H0318: 1, H0046: 1, H0457: 1, H0039: 1, H0553: 1, L0763: 1, L0761: 1, L0764: 1, L0789: 1, H0144: 1, S0374: 1, S0310: 1, H0555: 1, L0758: 1, H0445: 1 and S0276: 1. | | |

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| | | 894404 | 561 | 1 - 339 | 1174 | Val-14 to Lys-21, Gln-41 to Trp-46, Ala-98 to Pro-103. | | | | |
| 237 | HWLEA48 | 927676 | 247 | 100 - 408 | 860 | Pro-1 to Thr-8. | AR089: 1, AR061: 0 S0354: 1 and L0596: 1. | | | |
| 238 | HWLHS82 | 934505 | 248 | 2 - 427 | 861 | Gly-34 to Lys-44, Glu-113 to Glu-118. | AR089: 2, AR061: 1 L0769: 3, S0354: 1, H0393: 1, H0355: 1 and H0124: 1. | | | |
| 239 | HWMIB81 | 955336 | 249 | 1491 - 922 | 862 | Ile-94 to Asp-99, Asp-118 to Pro-123, Glu-131 to Ile-140, Tyr-143 to Asp-152, Glu-169 to Lys-179. | AR061: 1, AR089: 1 L0748: 2, H0171: 1, S0134: 1, S0354: 1, S0358: 1, H0014: 1, H0083: 1, H0510: 1, L0764: 1, L0803: 1, L0789: 1, H0593: 1, H0659: 1, H0539: 1, H0555: 1, L0751: 1, L0758: 1, L0759: 1 and L0595: 1. | | | |
| 240 | HCWDV17 | 1105673 | 250 | 32 - 607 | 863 | Ala-144 to Glu-151, Thr-162 to Thr-168. | AR089: 12, AR061: 6 H0305: 4 | | | |
| | | 974478 | 562 | 32 - 697 | 1175 | Ala-144 to Glu-151, Thr-162 to Thr-168. | | | | |
| 241 | HELDI95 | 1103374 | 251 | 49 - 525 | 864 | | AR089: 1, AR061: 1 S0045: 2, S0278: 1, | | | |

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| | | | | | | | | | H0191: 1, H0027: 1, H0644: 1, S0028: 1, S0031: 1 and S0260: 1. | | | |
| 242 | HAGFO25 | 953059 1150845 | 563 252 | 461 - 895 1 - 735 | 1176 865 | Arg-71 to Asp-76. Gly-1 to Glu-7, Gly-30 to Gln-40, Gly-69 to Gln-75, Leu-98 to Leu-107, Tyr-146 to Gly-161, Arg-179 to Ser-186. | AR061: 9, AR089: 3 L0794: 11, S0010: 3, S0346: 3, L0791: 2, L0439: 2, L0758: 2, S0222: 1, T0060: 1, H0051: 1, S0388: 1, H0188: 1, S0214: 1, H0252: 1, L0666: 1, L0438: 1, L0743: 1, L0750: 1, L0779: 1, S0031: 1, L0480: 1, L0597: 1 and H0667: 1. | | | | | |
| 243 | HAWAB54 | 957992 1149319 | 564 253 | 3 - 728 1440 - 283 | 1177 866 | Gly-26 to Gln-36, Gly-65 to Gln-71, Leu-94 to Leu-103. Ala-16 to Thr-21, Arg-76 to Asn-104, Ala-123 to Glu-129, Leu-142 to Glu-147, Gly-170 to Gln-180, Gly-209 to Gln-215, Leu-238 to Leu-247. | L0794: 11, S0010: 3, S0346: 3, L0791: 2, L0439: 2, L0758: 2, S0222: 1, T0060: 1, H0051: 1, S0388: 1, H0188: 1, S0214: 1, H0252: 1, L0666: 1, | | | | | |

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| 244 | HLIBV06 | 957993 | 565 | 9 - 374 | 1178 | Arg-1 to Arg-6. | Tyr-286 to Gly-301, Arg-319 to Ser-326. | L0438: 1, L0743: 1, L0750: 1, L0779: 1, S0031: 1, L0480: 1, L0597: 1 and H0667: 1. | | |
| | | 934887 | 254 | 3 - 350 | 867 | Arg-1 to Thr-6, Pro-8 to Arg-24, Glu-30 to Lys-35. | | AR089: 4, AR061: 2 L0752: 13, L0777: 10, H0663: 7, L0803: 7, L0731: 7, S0356: 6, H0441: 6, L0766: 6, L0758: 6, L0646: 5, L0659: 5, L0485: 5, H0586: 4, H0031: 4, H0553: 4, L0521: 4, L0664: 4, H0660: 4, S0378: 4, L0740: 4, L0754: 4, L0756: 4, H0431: 3, H0615: 3, H0673: 3, S0040: 2, S0354: 2, S0360: 2, H0369: 2, H0331: 2, T0040: 2, H0318: 2, L0471: 2, H0197: 2, H0428: 2, L0770: 2, L0662: 2, L0774: 2, L0651: 2, L0666: 2, | | |

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| | S0374: 2, S0126: 2, H0518: 2, H0555: 2, L0747: 2, L0750: 2, L0759: 2, S0031: 2, L0591: 2, H0506: 2, H0352: 2, L0615: 1, H0685: 1, S0114: 1, S0358: 1, S0376: 1, H0637: 1, H0580: 1, H0411: 1, H0592: 1, H0632: 1, T0039: 1, S0280: 1, H0156: 1, L0021: 1, H0599: 1, H0098: 1, T0048: 1, S0474: 1, H0421: 1, H0251: 1, H0263: 1, H0596: 1, H0597: 1, H0231: 1, H0009: 1, H0199: 1, H0246: 1, H0057: 1, H0014: 1, H0355: 1, H0510: 1, H0379: 1, H0059: 1, H0494: 1, S0464: 1, S0466: 1, H0509: 1, H0641: 1, H0647: 1, L0369: 1, L0772: 1, | |
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| 245 | HMALL66 | 1105097 | 255 | 38 - 376 | 868 | Gln-54 to Val-63, Asn-88 to Pro-93. | AR061: 9, AR089: 3 L0770: 4, H0638: 1, S0278: 1, H0641: 1, L0763: 1, L0809: 1, L0779: 1 and L0758: 1. | L0771: 1, L0804: 1, L0805: 1, L0776: 1, L0657: 1, L0382: 1, L0809: 1, L0663: 1, L0665: 1, H0144: 1, H0691: 1, T0068: 1, H0520: 1, H0658: 1, H0648: 1, H0539: 1, H0521: 1, S0028: 1, L0744: 1, L0748: 1, L0779: 1, L0592: 1, L0604: 1, L0362: 1 and S0276: 1. | | |
| | | 956195 | 566 | 39 - 377 | 1179 | Gln-54 to Val-63, Asn-88 to Pro-93. | | | | |
| 246 | HOACE12 | 858976 | 256 | 2 - 349 | 869 | | AR089: 2, AR061: 1 L0794: 11, S0010: 3, S0346: 3, L0791: 2, L0439: 2, L0758: 2, S0222: 1, T0060: 1, H0051: 1, S0388: 1, | | | |

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| | | | | | | | | | H0188: 1, S0214: 1, H0252: 1, L0666: 1, L0438: 1, L0743: 1, L0750: 1, L0779: 1, S0031: 1, L0480: 1, L0597: 1 and H0667: 1. | | |
| 247 | HOGCG69 | 924848 | 257 | 480 - 1187 | 870 | Asn-29 to Gly-39, Pro-49 to Asn-56, Gln-112 to Ala-119, Arg-193 to Gln-201, Leu-222 to Gln-227. | | | AR089: 36, AR061: 2 H0616: 2, H0618: 1, H0604: 1, H0063: 1 and H0435: 1. | | |
| 248 | HAGAE09 | 1150864 | 258 | 852 - 565 | 871 | Ser-47 to His-52. | | | AR061: 1, AR089: 1 L0005: 1, H0438: 1, S0010: 1, L0665: 1, H0444: 1 and L0594: 1. | | |
| 249 | HAGAE34 | 1121869 | 259 | 48 - 206 193 - 480 | 872 | Leu-16 to Ser-32. Phe-7 to Glu-13, Gln-46 to Thr-59. | | | AR089: 10, AR061: 8 L0439: 2, S0010: 1, L0796: 1 and L0805: 1. | | |
| 250 | HARMH78 | 525878 1137572 | 568 260 | 83 - 322 560 - 3 | 1181 873 | | | | AR089: 13, AR061: 5 S0360: 1, H0592: 1 and H0087: 1. | | |
| 251 | HBJLB53 | 773210 1226988 | 569 261 | 87 - 284 1150 - 869 | 1182 874 | Gln-24 to Arg-44. Asn-8 to Thr-14, Gly-38 to Gly-44, | | | AR089: 9, AR061: 8 H0318: 2, H0171: 1, | | |

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| | | | | | | | Lys-58 to Val-63, Tyr-71 to Val-78. | | | H0069: 1, H0123: 1, L0783: 1, H0521: 1 and L0748: 1. | | |
| 252 | HBJNB52 | 974122 | 570 | 298 - 450 | 1183 | | Gln-20 to Arg-26. | | | AR061: 4, AR089: 4 H0318: 1, L0766: 1 and L0748: 1. | | |
| | | 1128792 | 262 | 527 - 75 | 875 | | Leu-16 to Glu-22, Tyr-89 to Asn-95. | | | | | |
| 253 | HDABQ83 | 726475 | 571 | 160 - 357 | 1184 | | Pro-15 to Cys-23. | | | AR089: 4, AR061: 2 L0163: 3, H0497: 2, L0439: 2, H0662: 1, S0360: 1, L0717: 1, S6016: 1, S0051: 1, H0428: 1, L0662: 1, L0768: 1, L0774: 1, L0776: 1, L0656: 1, L0789: 1, L0666: 1, L0743: 1, L0749: 1 and L0777: 1. | | |
| | | 1201703 | 263 | 183 - 1 | 876 | | Lys-17 to Phe-26, Gln-30 to Leu-43. | | | | | |
| 254 | HDPDC84 | 669619 | 572 | 219 - 374 | 1185 | | Asp-3 to Ser-11. | | | AR061: 4, AR089: 1 L0749: 6, L0794: 5, H0550: 4, H0575: 4, H0521: 4, L0601: 4, H0580: 3, L0761: 3, L0766: 3, H0402: 2, | | |
| | | 1226990 | 264 | 82 - 2970 | 877 | | Lys-32 to Val-61, Pro-83 to Ala-89, Lys-114 to Gly-120, Asn-137 to Arg-147, Gly-186 to Thr-194, Val-211 to Glu-227, | | | | | |

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| Ile-236 to Glu-242, Phe-254 to Lys-264, Glu-328 to Leu-334, Phe-355 to Asn-379, Thr-434 to Leu-444, Glu-495 to Leu-502, Gln-533 to Lys-538, Ser-586 to Trp-594, Leu-605 to Glu-611, Pro-614 to Leu-624, Thr-626 to Gln-640, Ser-679 to Ala-684, Lys-750 to Gly-771, Glu-840 to Asp-853, Glu-866 to Glu-874, Ser-881 to Ala-915, Asn-929 to Gly-944, Ala-946 to Thr-953. | S0360: 2, H0549: 2, H0628: 2, H0264: 2, H0560: 2, S0002: 2, L0803: 2, L0787: 2, L0789: 2, S3014: 2, L0777: 2, L0752: 2, L0731: 2, H0423: 2, H0657: 1, S0212: 1, H0306: 1, H0589: 1, S0358: 1, S0046: 1, H0610: 1, H0391: 1, H0486: 1, H0250: 1, S0280: 1, H0318: 1, H0581: 1, H0309: 1, H0373: 1, H0030: 1, H0135: 1, H0038: 1, H0634: 1, H0272: 1, H0494: 1, H0509: 1, S0426: 1, L0662: 1, L0804: 1, L0775: 1, L0806: 1, L0659: 1, L0532: 1, H0547: 1, H0555: 1, S0432: 1, L0754: 1, L0747: 1, L0750: 1, L0779: 1, L0758: 1, S0031: 1, |
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| | | | | | | | | | | L0584: 1 and H0136: 1. | | |
| | | 616980 | 573 | 64 - 528 | 1186 | Lys-32 to Val-61, Pro-83 to Ala-89. | | | | | | |
| 255 | HDPUF40 | 1212494 | 265 | 49 - 1713 | 878 | Ala-9 to Glu-20, Thr-22 to Gly-32, Gly-57 to Ser-67, Arg-125 to Ser-138, Gly-167 to Gly-173, Ala-289 to Glu-298, Leu-317 to Ala-323, Glu-339 to Gly-347, Leu-358 to Thr-363, Glu-395 to Arg-411, Ser-446 to Glu-455, Glu-475 to Ala-481, Ser-489 to Leu-497, Ala-501 to Pro-512, Asn-520 to Asn-526, Ser-546 to Glu-553. | | | | AR089: 0, AR061: 0 H0436: 11, H0255: 7, H0559: 7, H0521: 7, H0254: 4, H0423: 4, H0265: 3, H0486: 3, H0250: 3, H0581: 3, H0271: 3, H0124: 3, H0264: 3, H0555: 3, H0341: 2, S0354: 2, H0580: 2, H0370: 2, H0586: 2, H0257: 2, H0069: 2, H0083: 2, H0031: 2, H0634: 2, H0488: 2, S0422: 2, S0426: 2, L0766: 2, L0649: 2, L0805: 2, L0653: 2, L0776: 2, L0655: 2, L0731: 2, H0445: 2, H0543: 2, H0677: 2, H0556: 1, H0584: 1, H0140: 1, H0583: 1, H0656: 1, H0402: 1, H0305: 1, | | |

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| 256 | HDPWU07 | 1228286 | 266 | 1036 - 1416 | 879 | Ala-9 to Glu-20, Thr-22 to Gly-32, Gly-57 to Ser-67, Arg-125 to Ser-138, Gly-167 to Gln-176. Ser-77 to His-82. | AR089: 2, AR061: 1 H0587: 3, L0664: 3, L0665: 3, H0648: 3, L0740: 3, H0581: 2, L0659: 2, H0539: 2, H0521: 2, L0750: 2, | |
| | | 970586 | 574 | 49 - 705 | 1187 | | H0458: 1, S0140: 1, H0550: 1, H0497: 1, H0575: 1, S0474: 1, H0421: 1, H0024: 1, H0213: 1, H0087: 1, H0272: 1, H0641: 1, S0144: 1, L0763: 1, L0761: 1, L0662: 1, L0794: 1, L0803: 1, L0804: 1, L0659: 1, L0787: 1, L0666: 1, L0663: 1, H0518: 1, S0044: 1, H0576: 1, L0756: 1, H0422: 1, S0452: 1 and H0506: 1. | |

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| | | | | | | | | | L0777: 2, L0759: 2, H0423: 2, S0218: 1, H0661: 1, H0305: 1, H0459: 1, S0360: 1, H0580: 1, L0717: 1, H0486: 1, T0074: 1, H0036: 1, H0051: 1, S0388: 1, H0039: 1, H0553: 1, H0124: 1, H0412: 1, L0770: 1, L0662: 1, L0768: 1, L0766: 1, L0649: 1, L0775: 1, L0789: 1, L0791: 1, L0532: 1, S0216: 1, H0682: 1, H0659: 1, H0670: 1, S0270: 1, H0540: 1, L0747: 1, L0780: 1, L0755: 1, L0592: 1, L0581: 1, L0604: 1 and H0422: 1. | | | | | | | |
| | | 952734 | 575 | 297 - 446 | 1188 | | | | | | | | | | | |
| 257 | HDTJJ02 | 1106328 | 267 | 86 - 331 | 880 | Pro-47 to Gly-54. | | | | | | | AR089: 34, AR061: 11 H0486: 2 | | | |
| | | 913787 | 576 | 3 - 116 | 1189 | | | | | | | | | | | |
| 258 | HE2GA18 | 1121872 | 268 | 288 - 1 | 881 | Tyr-1 to Ser-10, | | | | | | | AR089: 1, AR061: 1 | | | |

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| 261 | HFIYW31 | 934511 | 579 | 1 - 576 | 1192 | Asn-128 to Ser-139, Glu-163 to Thr-168, Leu-172 to Ser-182. | H0144: 1, H0593: 1, S0126: 1, H0658: 1, H0660: 1, H0539: 1, H0555: 1, S3014: 1, L0777: 1, L0731: 1, H0445: 1, L0588: 1, H0542: 1, H0506: 1 and H0352: 1. | | |
| | | 1151476 | 271 | 521 - 288 | 884 | Lys-7 to Thr-16, Lys-33 to Asn-41, Glu-52 to Arg-63. | AR089: 2, AR061: 1 L0809: 7, L0771: 6, L0766: 6, S0360: 5, L0805: 4, L0748: 4, H0674: 3, L0776: 3, L0756: 3, L0779: 3, L0770: 2, L0794: 2, L0518: 2, L0666: 2, L0439: 2, L0740: 2, L0749: 2, L0608: 2, S0242: 2, H0556: 1, H0306: 1, S0358: 1, S0376: 1, H0438: 1, H0597: 1, S6028: 1, S0036: 1, T0041: 1, | | |

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| | | | | | | Asn-124 to Leu-133. | L0755: 2, L0759: 2, S0342: 1, S6024: 1, S0376: 1, L0021: 1, H0150: 1, T0003: 1, H0014: 1, L0764: 1, L0794: 1, L0803: 1, L0783: 1, L0809: 1, L0666: 1, L0665: 1, L0438: 1, L0749: 1, L0779: 1, L0777: 1, L0758: 1, L0604: 1, S0026: 1 and H0423: 1. | | |
| | | | | | | Asn-18 to Arg-23. | AR089: 7, AR061: 3 L0731: 3, H0395: 2, L0764: 2, L0794: 2, H0521: 2, T0049: 1, H0650: 1, S0140: 1, L0021: 1, H0083: 1, H0271: 1, L0769: 1, L0761: 1, L0646: 1, L0771: 1, L0803: 1, L0804: 1, L0775: 1, L0519: 1, H0445: 1, L0588: 1 and H0542: 1. | | |
| | | | | | | Pro-109 to Ser-114, Arg-146 to Arg-153. | | | |
| 264 | HHEBB62 | 771320 | 582 | 274 - 426 | 1195 | Ser-47 to Thr-54, Asn-62 to Asp-67, Pro-109 to Ser-114, Arg-146 to Arg-153. | | | |
| | | 1151481 | 274 | 459 - 1 | 887 | | | | |
| | | 791469 | 583 | 529 - 158 | 1196 | Pro-27 to Lys-34, | | | |

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|-----|---------|---------|-----|-----------|------|--|---|-------------|---|--|
| 265 | HHEHU73 | 1151483 | 275 | 378 - 746 | 888 | Glu-49 to Asn-59, Lys-70 to Lys-82, Gly-99 to Cys-116. | AR089: 64, AR061: 15 H0542: 2 | | | |
| | | 923895 | 584 | 61 - 279 | 1197 | Glu-4 to Leu-11, Gln-30 to Cys-40, Pro-53 to Pro-59, Thr-99 to Ser-104. | | | | |
| 266 | HHEMA11 | 1151484 | 276 | 129 - 497 | 889 | Gln-13 to Ile-29. | AR089: 3, AR061: 1 H0328: 1, L0758: 1 and H0543: 1. | | | |
| | | 966924 | 585 | 129 - 497 | 1198 | Gln-13 to Ile-29. | | | | |
| 267 | HHEQK01 | 1107392 | 277 | 195 - 1 | 890 | Gln-1 to Thr-6. | AR089: 7, AR061: 1 L0589: 1, H0542: 1 and H0543: 1. | | | |
| | | 871911 | 586 | 64 - 249 | 1199 | | | | | |
| 268 | HHPEM84 | 915639 | 278 | 2 - 373 | 891 | | AR089: 68, AR061: 29 | 20q11.2-q12 | 139190, 139190, 224100, 600281, 600281, 601002, 601002, 601146, 601146, 601146 | |

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| 269 | HHSED84 | 1150832 | 279 | 632 - 3 | 892 | Asp-73 to Ser-80, Arg-104 to Asp-115, Glu-195 to Pro-202. | AR061: 8, AR089: 4 L0748: 5, L0744: 4, L0751: 4, H0039: 3, H0617: 3, L0646: 3, L0809: 3, L0779: 3, H0295: 2, H0255: 2, S0358: 2, H0575: 2, H0457: 2, H0181: 2, H0673: 2, L0637: 2, L0743: 2, L0750: 2, L0758: 2, S0116: 1, H0663: 1, S0356: 1, S0376: 1, S0360: 1, H0675: 1, S0007: 1, H0497: 1, H0590: 1, H0618: 1, H0253: 1, H0545: 1, S0051: 1, H0622: 1, H0030: 1, H0135: 1, H0538: 1, S0426: 1, H0529: 1, L0763: 1, L0769: 1, L0764: 1, L0771: 1, L0773: 1, L0775: 1, L0788: 1, L0663: 1, H0144: 1, L0438: 1, H0690: 1, H0670: 1, | | |
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| 270 | HIBCC94 | | | | | | | | H0672: 1, S0328: 1, S0406: 1, H0187: 1, L0747: 1, L0749: 1, L0759: 1 and L0608: 1. | | |
| | | 706739 | 587 | 2 - 496 | 1200 | Asn-1 to Asp-8, Gly-51 to Ser-64. | | | | | |
| | | 1161292 | 280 | 806 - 258 | 893 | Cys-12 to Gln-17, Lys-47 to Thr-57, Leu-77 to Gly-92, Gln-153 to Arg-160. | | | AR089: 1, AR061: 1 L0439: 4, T0010: 1 and L0352: 1. | | |
| | | 504326 | 588 | 3 - 251 | 1201 | Glu-1 to Arg-6, Ser-11 to Val-17, Gln-42 to Arg-54. | | | | | |
| 271 | HKADN56 | 504330 | 589 | 470 - 132 | 1202 | | | | | | |
| | | 1220254 | 281 | 370 - 1650 | 894 | Ser-32 to Glu-39, Ala-60 to Trp-69. | | | AR089: 7, AR061: 4 L0754: 12, S0360: 8, S0152: 7, S0358: 6, H0046: 6, H0100: 5, L0751: 5, L0777: 5, L0601: 5, H0052: 4, L0740: 4, H0051: 3, H0266: 3, L0526: 3, S0374: 3, L0779: 3, H0265: 2, H0556: 2, H0341: 2, H0661: 2, H0619: 2, H0050: 2, | | |
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| | | | | | H0188: 1, H0290: 1, H0252: 1, H0328: 1, H0424: 1, H0213: 1, H0031: 1, H0553: 1, H0032: 1, H0674: 1, H0361: 1, H0135: 1, H0038: 1, H0551: 1, H0264: 1, H0412: 1, H0059: 1, H0494: 1, H0561: 1, S0142: 1, S0344: 1, S0210: 1, S0002: 1, L0769: 1, L0644: 1, L0773: 1, L0767: 1, L0766: 1, L0776: 1, L0542: 1, L0783: 1, L0382: 1, L0530: 1, L0367: 1, L0790: 1, L0666: 1, L0663: 1, L0664: 1, L0665: 1, H0144: 1, H0520: 1, H0547: 1, H0593: 1, H0666: 1, H0696: 1, H0436: 1, L0747: 1, L0749: 1, L0757: 1, H0445: 1, H0707: 1, L0596: 1, |
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| 275 | HLYDC50 | 1151494 | 285 | 2 - 874 | 898 | Ser-1 to Ser-10, Ser-23 to Asp-38, Arg-67 to Lys-73, Ser-181 to Asp-187, Asp-222 to Ser-233, Pro-248 to Asn-253. | AR061: 4, AR089: 3, L0766: 5, L0806: 3, T0010: 2, L0761: 2, L0752: 2, H0677: 2, S0278: 1, H0486: 1, S0038: 1, L0796: 1, | | | | L0731: 3, S0026: 3, S0422: 2, L0764: 2, L0655: 2, L0606: 2, L0665: 2, L0439: 2, L0759: 2, S0114: 1, H0650: 1, H0369: 1, H0600: 1, H0581: 1, H0421: 1, H0271: 1, H0615: 1, H0591: 1, H0038: 1, H0040: 1, H0063: 1, H0494: 1, L0598: 1, L0520: 1, L0761: 1, L0662: 1, L0767: 1, L0649: 1, L0803: 1, L0775: 1, L0805: 1, L0809: 1, L0664: 1, L0438: 1, H0658: 1, H0672: 1, H0436: 1, L0747: 1 and S0196: 1. | | |
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| | | | | | | | | | L0644: 1, L0771: 1, L0659: 1, L0666: 1, L0664: 1, H0521: 1, L0779: 1, H0445: 1 and L0595: 1. | | |
| | | 677050 | 593 | 2 - 424 | 1206 | Ser-1 to Ser-10, Ser-23 to Asp-38. | | | | | |
| 276 | HMADD49 | 1217031 | 286 | 2227 - 803 | 899 | Pro-45 to Ser-50, Thr-54 to Ile-64, Lys-205 to Arg-211, Pro-214 to Gly-220, Asp-296 to Asp-301, Pro-355 to Glu-367, Thr-391 to Glu-396. | | | AR061: 77, AR089: 30 S0136: 3, S0036: 1 and S0144: 1. | | |
| | | 867481 | 594 | 2 - 283 | 1207 | Leu-33 to Phe-38. | | | | | |
| 277 | HMEKE78 | 1128290 | 287 | 80 - 1339 | 900 | Pro-39 to Glu-45, Pro-102 to Arg-107, Tyr-121 to Lys-128, Gln-140 to Ile-169, Arg-269 to Gly-285, Lys-313 to Gly-320, Ala-344 to Thr-350, Arg-356 to Gln-365, Tyr-373 to His-380, Arg-392 to Leu-399, Leu-403 to Gln-408. | | | AR061: 10, AR089: 5 S0328: 4, S0218: 3, H0040: 2, L0438: 2, L0439: 2, H0624: 1, H0431: 1, L0021: 1, S0049: 1, H0266: 1, H0090: 1, H0561: 1, S0422: 1, H0529: 1, L0659: 1, S0126: 1, S0027: 1, S0028: 1, S0206: 1, L0748: 1, | | |

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| 278 | HMSHU26 | 792383 | 595 | 3 - 461 | 1208 | Phe-3 to Phe-8, Pro-30 to Glu-36, Pro-93 to Arg-98. | L0731: 1, S0031: 1, L0596: 1, L0608: 1 and S0011: 1. | | |
| | | 1150833 | 288 | 993 - 703 | 901 | Ser-41 to Glu-47, Arg-71 to Leu-85, Asp-87 to Glu-97. | | | |
| 279 | HNEEB82 | 681745 | 596 | 29 - 235 | 1209 | Glu-15 to His-24, Asn-47 to His-53. | AR061: 5, AR089: 4 L0748: 2, H0191: 1, H0100: 1, S0002: 1, L0646: 1, L0794: 1, L0806: 1 and L0758: 1. | | |
| | | 1076509 | 289 | 261 - 1 | 902 | Gln-1 to Gly-7, Ser-63 to Gly-68, Pro-74 to Cys-81. | | | |
| | | 778884 | 597 | 30 - 260 | 1210 | Glu-1 to Glu-22. | | | |
| 280 | HNHIA06 | 1162086 | 290 | 605 - 159 | 903 | Asp-29 to Arg-35, Leu-58 to Thr-64. | AR089: 3, AR061: 3 S0282: 1 and S0053: 1. | | |
| | | 859932 | 598 | 120 - 566 | 1211 | Asp-29 to Arg-35, Leu-58 to Thr-64. | | | |
| 281 | HODFY16 | 1105244 | 291 | 370 - 221 | 904 | Ile-34 to Gly-42. | AR061: 6, AR089: 3 H0615: 2 and L0766: 1. | | |
| | | 958329 | 599 | 163 - 309 | 1212 | | | | |

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|-----|---------|---------|-----|-----------|------|--|---|--|--|--|
| 282 | HPQSB68 | 1221022 | 292 | 294 - 97 | 905 | Asp-36 to Lys-42. | AR089: 1, AR061: 1 S0136: 2 | | | |
| | | 740087 | 600 | 89 - 247 | 1213 | Leu-7 to Gln-17. | | | | |
| 283 | HRDBH04 | 1150876 | 293 | 329 - 724 | 906 | Thr-56 to Gly-62, Glu-72 to Gly-81. | AR089: 7, AR061: 6 L0769: 16, L0776: 16, L0742: 13, L0745: 13, L0754: 12, L0748: 11, L0439: 11, L0747: 10, L0805: 8, L0438: 6, L0731: 6, L0764: 5, L0806: 5, L0749: 5, L0779: 5, L0752: 5, L0771: 4, H0052: 3, L0796: 3, L0761: 3, L0741: 3, L0756: 3, L0753: 3, L0758: 3, S0360: 2, H0013: 2, H0068: 2, T0041: 2, L0768: 2, L0659: 2, L0783: 2, L0809: 2, H0670: 2, L0746: 2, L0591: 2, H0265: 1, H0686: 1, H0583: 1, H0657: 1, L0785: 1, H0662: 1, S0418: 1, | | | |

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| | | | | | | | | | L0743: 1, L0777: 1, L0780: 1, L0755: 1, L0757: 1, L0759: 1, L0603: 1, S0026: 1, H0543: 1 and H0352: 1. | | |
| 284 | HSICR69 | 922022 | 601 | 285 - 680 | 1214 | Thr-56 to Gly-62, Glu-72 to Gly-81. | | | AR089: 2, AR061: 1 H0036: 2 | | |
| 285 | HSIGJ94 | 1226965 | 294 | 547 - 29 | 907 | Thr-48 to Arg-54, Pro-149 to Ser-155. | | | AR061: 8, AR089: 7 H0590: 1, L0766: 1, L0659: 1, L0608: 1 and L0362: 1. | | |
| 286 | HSYBL15 | 793624 | 603 | 117 - 284 | 1216 | | | | AR061: 1, AR089: 0 S0212: 1, H0551: 1 and L0366: 1. | | |
| 287 | HTEKH29 | 1104299 | 296 | 2 - 931 | 909 | Pro-26 to Gly-32, Ala-133 to Cys-138, Asp-145 to Lys-152, Leu-164 to Ser-173, Lys-178 to Ser-183, Asp-260 to Phe-266. | | | | | |
| | | 660053 | 604 | 2 - 286 | 1217 | Pro-26 to Gly-32. | | | | | |
| | | 855660 | 297 | 478 - 2028 | 910 | Ser-27 to Glu-35, Thr-43 to Phe-52, Val-59 to Gln-70, His-74 to Val-79. | | | AR089: 8, AR061: 7 | | |

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| | | | | | | | Pro-108 to Lys-122, Ala-130 to Phe-141, Val-145 to Ala-151, Asp-159 to Glu-165, Ser-185 to Lys-191. | | | | | |
| 288 | HTGEL46 | 1151520 | 298 | 331 - 705 | 911 | | Glu-55 to His-72. | | AR089: 0, AR061: 0 S0218: 1, H0264: 1 and S0053: 1. | | | |
| | | 685425 | 605 | 323 - 457 | 1218 | | | | | | | |
| 289 | HTGFA05 | 1198110 | 299 | 3 - 1262 | 912 | | Ile-45 to Arg-52, Phe-77 to Pro-85, Leu-111 to Val-118, Ile-124 to Thr-129, Pro-139 to Gly-151, Arg-186 to Gly-215, Lys-223 to Glu-230. | | AR061: 1, AR089: 0 H0556: 10, L0748: 8, H0620: 7, L0747: 7, L0637: 5, H0265: 4, H0013: 4, H0551: 4, L0776: 4, L0663: 4, L0596: 4, H0622: 3, H0617: 3, L0772: 3, L0766: 3, S0126: 3, L0751: 3, L0752: 3, S0031: 3, L0593: 3, H0657: 2, S0360: 2, S0222: 2, T0115: 2, H0009: 2, L0471: 2, H0594: 2, H0288: 2, H0039: 2, H0424: 2, H0135: 2, H0040: 2, | | | |

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| | | | | | S0038: 1, H0561: 1, S0352: 1, S0144: 1, S0142: 1, L0369: 1, L0761: 1, L0372: 1, L0646: 1, L0374: 1, L0764: 1, L0771: 1, L0773: 1, L0381: 1, L0388: 1, L0774: 1, L0651: 1, L0378: 1, L0657: 1, L0658: 1, L0383: 1, L0665: 1, L0352: 1, H0593: 1, H0689: 1, H0682: 1, H0660: 1, S0328: 1, H0696: 1, S0044: 1, S0037: 1, S3014: 1, S0206: 1, L0439: 1, L0754: 1, L0749: 1, L0750: 1, L0731: 1, L0759: 1, L0588: 1, L0362: 1, L0361: 1, H0653: 1, H0136: 1, S0196: 1, H0543: 1 and S0424: 1. | |
| 972982 | 606 | 1610 - 489 | 1219 | Arg-27 to Phe-33, Phe-43 to Gly-51, | | |

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| 290 | HTLDU61 | 1165319 | 300 | 690 - 220 | 913 | Cys-59 to Thr-68, Ile-78 to Thr-83, Pro-93 to Gly-105, Arg-140 to Gly-169, Lys-177 to Glu-184. | AR061: 2, AR089: 2 H0253: 1, S0010: 1, L0456: 1, H0695: 1 and L0657: 1. | | |
| | | 530316 | 607 | 63 - 224 | 1220 | Gln-5 to His-17, Pro-30 to Ser-40, Pro-42 to Thr-65, Gly-102 to Gln-107, Ala-112 to Lys-118, Ser-127 to Thr-138. | | | |
| 291 | HTOFT34 | 1152490 | 301 | 361 - 609 | 914 | | AR089: 8, AR061: 5 H0264: 2 and L0367: 1. | | |
| | | 527144 | 608 | 106 - 270 | 1221 | | | | |
| 292 | HTTDH46 | 1152491 | 302 | 2 - 1144 | 915 | Gly-50 to Asp-59, Thr-220 to Phe-233, Glu-285 to Tyr-291, Thr-298 to Arg-303, Ala-353 to Asn-358. | AR061: 7, AR089: 2 H0253: 10, H0617: 8, H0559: 7, H0265: 6, H0618: 5, H0551: 5, H0052: 4, H0620: 4, L0794: 4, H0556: 3, H0135: 3, H0087: 3, L0659: 3, L0666: 3, L0663: 3, L0438: 3, H0522: 3, L0749: 3, | | |

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| | H0581: 1, H0194: 1, H0327: 1, H0046: 1, H0009: 1, H0178: 1, H0012: 1, H0023: 1, H0201: 1, S0051: 1, H0083: 1, S6028: 1, H0266: 1, H0271: 1, H0428: 1, H0604: 1, H0417: 1, H0181: 1, H0163: 1, H0038: 1, H0634: 1, H0063: 1, H0264: 1, H0412: 1, S0038: 1, L0351: 1, H0359: 1, S0150: 1, H0646: 1, H0538: 1, S0002: 1, S0426: 1, L0640: 1, L0772: 1, L0372: 1, L0641: 1, L0643: 1, L0764: 1, L0767: 1, L0768: 1, L0766: 1, L0375: 1, L0378: 1, L0806: 1, L0652: 1, L0656: 1, L0636: 1, L0790: 1, L0664: 1, H0144: 1, S0374: 1, H0520: 1, | |
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| 293 | HTTIO05 | 951114 | 609 | 3 - 500 | 1222 | Arg-1 to Thr-15. | H0547: 1, H0593: 1, H0682: 1, H0651: 1, S0328: 1, H0539: 1, S0380: 1, S0332: 1, S3014: 1, S0027: 1, L0754: 1, L0750: 1, L0755: 1, L0757: 1, L0758: 1, S0031: 1, L0593: 1, H0667: 1, H0217: 1, H0423: 1, H0422: 1 and S0042: 1. | | |
| | | 1229905 | 303 | 1367 - 1624 | 916 | | AR061: 57, AR089: 49 L0770: 2, S0114: 1, L0717: 1, H0634: 1, L0773: 1, L0521: 1, L0803: 1, L0791: 1, L0664: 1, S0330: 1, S0380: 1, L0759: 1 and H0653: 1. | | |
| 294 | HWHGY45 | 931037 | 610 | 1286 - 1564 | 1223 | | AR089: 23, AR061: 3 S0144: 2, H0662: 1, H0586: 1, H0587: 1, T0060: 1, H0696: 1 and L0745: 1. | | |
| | | 911621 | 304 | 3 - 203 | 917 | | | | |

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| 295 | HWLQR48 | 1128304 | 305 | 338 - 508 | 918 | | AR089: 23, AR061: 6 L0518: 4, L0731: 3, L0637: 2, H0659: 2, H0170: 1, S6024: 1, S0360: 1, H0586: 1, H0050: 1, L0598: 1, L0763: 1, L0666: 1, L0663: 1, L0743: 1, L0745: 1 and L0601: 1. | | |
| 296 | HWLQX76 | 914556 | 611 | 338 - 475 | 1224 | | Gly-1 to Pro-6, His-18 to Ser-23, Asn-45 to Thr-56, Ala-65 to Arg-70, Asp-84 to Ile-89, Glu-109 to Leu-114, Lys-146 to Lys-155. His-12 to Ser-17, Asn-39 to Thr-50, Ala-59 to Arg-64, Asp-78 to Ile-83. | AR089: 1, AR061: 1 H0553: 3, S0360: 1, H0561: 1, L0526: 1, H0519: 1, S0126: 1, H0543: 1 and L0697: 1. | |
| | | 1152280 | 306 | 2 - 466 | 919 | | | | |
| | | 894607 | 612 | 1 - 996 | 1225 | | | | |
| 297 | HATDD09 | 1165331 | 307 | 428 - 1027 | 920 | | AR061: 4, AR089: 4 L0361: 2, H0662: 1, T0039: 1, H0156: 1, H0052: 1, H0194: 1, H0179: 1, H0135: 1, | | |

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| | | | | | | | | | L0662: 1, L0364: 1, L0790: 1, L0666: 1, S0028: 1 and S0194: 1. | | |
| 298 | HBJGT03 | 573794 | 613 | 2 - 184 | 1226 | | | | AR061: 5, AR089: 3 L0769: 2, H0318: 1 and L0787: 1. | | |
| | | 1105484 | 308 | 352 - 89 | 921 | | | Ser-33 to Ala-47. | | | |
| | | 923800 | 614 | 35 - 226 | 1227 | | | Ala-16 to Ser-22, Pro-31 to Leu-38, Ser-41 to Gly-48. | | | |
| 299 | HMTMF45 | 1141737 | 309 | 33 - 401 | 922 | | | | AR061: 1, AR089: 1 L0766: 3, L0777: 2, S0116: 1, S0376: 1, H0457: 1, L0771: 1, L0803: 1, L0804: 1, L0657: 1, L0659: 1, H0525: 1 and L0750: 1. | | |
| | | 553382 | 615 | 2 - 376 | 1228 | | | Arg-3 to Asp-14, Glu-53 to Gly-59, Asp-105 to Asn-113. | | | |
| 300 | HHPDV86 | 522953 | 310 | 1 - 636 | 923 | | | Thr-6 to Asp-14, Ser-36 to Glu-41, Ala-159 to Trp-168, Ser-176 to Lys-181. | AR061: 7, AR089: 3 L0809: 3, L0747: 3, S0360: 2, H0422: 2, H0556: 1, S0040: 1, H0664: 1, S0358: 1, T0048: 1, H0051: 1, | | |

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| 301 | HE8BT56 | 732602 | 311 | 45 - 377 | 924 | | | L0794: 1, L0791: 1, L0664: 1, S0052: 1, S0053: 1, H0701: 1, H0689: 1, H0690: 1, H0521: 1, H0626: 1 and L0595: 1. | | |
| 302 | HUJDH06 | 907613 | 312 | 304 - 672 | 925 | Pro-10 to Lys-22. | | AR061: 3, AR089: 2 L0766: 7, L0439: 3, L0749: 3, H0013: 2, L0776: 2, L0740: 2, L0746: 2, H0083: 1, H0366: 1, S0422: 1, L0787: 1, L0791: 1, L0779: 1, L0780: 1 and L0752: 1. | | |
| 303 | HOEJG61 | 907614 | 313 | 174 - 671 | 926 | Lys-31 to Ser-37, Leu-112 to Ser-119. | | AR089: 1, AR061: 1 H0650: 1, H0591: 1 and S0390: 1. | | |
| 304 | HE8PN24 | 907620 | 314 | 2 - 724 | 927 | Gly-59 to Glu-66, Cys-87 to Asn-93, Asn-122 to Trp-127, | | AR061: 7, AR089: 2 L0769: 3, L0766: 2, L0638: 1, S0126: 1, H0683: 1, L0745: 1 and H0506: 1. | | |
| | | | | | | | | AR061: 2, AR089: 0 H0013: 2, S0142: 2, L0740: 1 and L0747: 1. | | |

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| 305 | HGBHI37 | 909745 | 315 | 2 - 451 | 928 | Arg-129 to Ser-134, Ala-144 to Asp-149, Asn-176 to Ala-182. | Ala-1 to Gly-10. | AR089: 1, AR061: 1 H0656: 1 and H0014: 1. | | | |
| 306 | HCHOK82 | 909755 | 316 | 1 - 1089 | 929 | Leu-52 to Leu-66, Trp-97 to Leu-103. | | AR089: 4, AR061: 3 H0457: 3, H0271: 3, H0543: 3, H0422: 2, H0583: 1, H0650: 1, H0484: 1, H0483: 1, S0442: 1, H0580: 1, S0140: 1, H0486: 1, H0250: 1, H0050: 1, H0630: 1, H0264: 1, H0488: 1, H0487: 1, S0002: 1, L0439: 1, H0707: 1, H0136: 1 and H0677: 1. | | | |
| 307 | HFPCH24 | 912608 | 317 | 2 - 352 | 930 | Thr-5 to Asn-13, Pro-69 to Ala-76. | | AR061: 3, AR089: 3 L0803: 3, S0222: 1, L0021: 1, H0510: 1, L0774: 1, L0777: 1, L0731: 1, S0260: 1 and S0434: 1. | | | |
| 308 | HTTKF86 | 912689 | 318 | 2 - 223 | 931 | Arg-9 to Pro-16. | | AR061: 4, AR089: 3 | 22q13.1 | 103050, | |

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| 309 | HCESA79 | 912709 | 319 | 25 - 315 | 932 | Glu-42 to Arg-55, Lys-63 to Gly-68. | AR061: 6, AR089: 2 H0194: 2, L0748: 2, H0052: 1, T0010: 1, H0658: 1, S0380: 1 and L0366: 1. | H0634: 1 and H0522: 1. | 103050, 124030, 124030, 138981, 182380, 188826, 190040, 190040, 190040 |
| | | | | | | | | | 141750, 141800, 141800, 141800, 141800, 141800, 141850, 141850, 141850, 141850, 141850, 156850, 186580, 191092, 600140, 600273, 601313, 601785 |

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| 310 | HDTBJ28 | 912714 | 320 | 533 - 243 | 933 | | AR089: 38, AR061: 25 H0393: 1 and H0486: 1. | | |
| 311 | HDPBF48 | 912783 | 321 | 3 - 809 | 934 | Asp-52 to Thr-62, Thr-101 to Trp-112, Gly-131 to Asn-141, Asp-173 to Ile-179. | AR089: 8, AR061: 3 L0758: 4, H0521: 3, L0163: 2, L0783: 2, L0749: 2, S0342: 1, L0021: 1, H0318: 1, H0373: 1, H0083: 1, H0674: 1, H0494: 1, H0529: 1, L0768: 1, L0790: 1, H0519: 1, S0126: 1, H0670: 1, L0602: 1, L0748: 1, L0777: 1, L0752: 1, L0759: 1, L0588: 1, H0542: 1 and H0422: 1. | | |
| 312 | HTPFY55 | 912928 | 322 | 117 - 563 | 935 | Val-14 to Val-19, Ser-27 to Ser-32. | AR089: 3, AR061: 2 H0039: 1, H0622: 1 and H0644: 1. | | |
| 313 | HMSCM47 | 923632 | 323 | 2 - 685 | 936 | Gln-13 to Lys-19, Gln-59 to Tyr-69, Asp-116 to His-126, Gly-164 to Lys-170, Gln-182 to Gly-187, Tyr-207 to Gly-212. | AR089: 6, AR061: 3 H0521: 3, L0794: 2, L0805: 2, H0520: 2, L0602: 2, L0756: 2, H0170: 1, H0556: 1, S0134: 1, S0116: 1, | | |

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| | H0341: 1, H0662: 1, S0354: 1, S0360: 1, H0580: 1, H0619: 1, S0278: 1, H0574: 1, H0599: 1, H0590: 1, H0596: 1, L0471: 1, H0024: 1, H0014: 1, L0163: 1, H0051: 1, H0510: 1, H0615: 1, H0644: 1, H0617: 1, H0068: 1, L0060: 1, H0551: 1, S0450: 1, S0002: 1, L0369: 1, L0763: 1, L0371: 1, L0631: 1, L0637: 1, L0800: 1, L0764: 1, L0363: 1, L0767: 1, L0549: 1, L0803: 1, L0774: 1, L0776: 1, L0809: 1, L0791: 1, H0144: 1, H0658: 1, H0522: 1, H0478: 1, S3014: 1, S0028: 1, L0747: 1, L0749: 1, L0752: 1, L0753: 1, L0731: 1, L0758: 1, | | | | | | |
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| 314 | HOOQA56 | 925132 | 324 | 234 - I | 937 | Arg-5 to His-10, Ser-40 to Gln-48. | L0759: 1, L0601: 1, L0366: 1 and H0506: 1. AR089: 2, AR061: 2 H0521: 8, H0457: 6, H0494: 4, L0439: 4, S0152: 3, S0206: 3, H0013: 2, H0551: 2, H0623: 2, L0789: 2, L0438: 2, S0027: 2, L0601: 2, H0556: 1, S0040: 1, H0675: 1, H0645: 1, H0393: 1, H0411: 1, H0549: 1, H0592: 1, H0250: 1, H0575: 1, H0581: 1, H0266: 1, H0628: 1, H0598: 1, H0038: 1, H0413: 1, H0056: 1, H0561: 1, S0150: 1, H0633: 1, H0647: 1, S0426: 1, H0529: 1, L0369: 1, L0766: 1, L0806: 1, H0703: 1, H0519: 1, H0522: 1, S0028: 1, L0740: 1, L0750: 1, S0031: 1. | | |
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| 315 | HTPCQ24 | 925349 | 325 | 1 - 450 | 938 | Gly-1 to Leu-26, Thr-28 to Leu-35. | L0595: 1 and S0011: 1. AR061: 2, AR089: 1 H0046: 21, L0747: 10, H0039: 3, H0024: 2, L0766: 2, L0654: 2, L0748: 2, L0439: 2, L0779: 2, L0777: 2, T0049: 1, S0212: 1, H0662: 1, S0354: 1, S0045: 1, H0393: 1, H0107: 1, H0266: 1, S0250: 1, H0615: 1, H0688: 1, H0040: 1, H0616: 1, H0551: 1, H0641: 1, L0770: 1, L0637: 1, L0764: 1, L0767: 1, L0768: 1, L0659: 1, L0647: 1, L0666: 1, S0027: 1, S0028: 1, L0743: 1, L0749: 1, L0750: 1, L0780: 1, L0755: 1, L0758: 1 and L0759: 1. | | |
| 316 | HWAEI37 | 929481 | 326 | 2 - 415 | 939 | | AR089: 5, AR061: 1 H0581: 1 and H0519: 1. | | |

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| 317 | HDPSF03 | 969536 | 327 | 1 - 1269 | 940 | | AR089: 9, AR061: 3 | | |
| 318 | HLHST63 | 581528 | 328 | 28 - 423 | 941 | Ala-1 to Gly-15, Arg-32 to Ser-38, Thr-62 to His-68, Ser-104 to Thr-110, Gly-117 to Thr-122. | L0731: 28, L0740: 22, L0747: 21, L0748: 20, S0003: 18, L0754: 17, L0438: 12, L0439: 12, L0775: 11, L0752: 11, S0026: 11, L0770: 10, H0521: 10, L0749: 9, S0358: 8, L0766: 8, L0659: 8, L0591: 8, S0192: 8, S0360: 7, L0764: 7, H0522: 7, S0010: 6, H0039: 6, S0002: 6, L0666: 6, L0665: 6, H0144: 6, S0126: 6, L0750: 6, L0755: 6, L0758: 6, S0426: 5, L0662: 5, L0663: 5, L0759: 5, L0599: 5, T0049: 4, S0282: 4, H0402: 4, S0354: 4, H0619: 4, H0620: 4, H0266: 4, H0032: 4, H0641: 4, S0422: 4, L0771: 4, | | |

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| | | | | | | L0776: 4, L0526: 4, L0664: 4, H0659: 4, L0751: 4, L0590: 4, L0608: 4, L0595: 4, H0305: 3, S0420: 3, S0376: 3, S0007: 3, S0045: 3, S0222: 3, H0441: 3, H0587: 3, S0414: 3, T0039: 3, H0013: 3, H0575: 3, L0483: 3, H0644: 3, H0124: 3, H0494: 3, H0538: 3, L0769: 3, L0372: 3, L0648: 3, L0521: 3, L0519: 3, S0374: 3, S0330: 3, S3014: 3, L0744: 3, L0757: 3, S0031: 3, L0485: 3, L0593: 3, L0362: 3, H0543: 3, H0170: 2, H0556: 2, H0657: 2, H0663: 2, H0580: 2, S6022: 2, H0369: 2, H0370: 2, H0427: 2, S0280: 2, H0036: 2, S0346: 2, |
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| 4.1446 E | 4.1447 E | 4.1448 E | 4.1449 E | 4.1450 E | 4.1451 E | 4.1452 E | 4.1453 E | 4.1454 E | 4.1455 E | 4.1456 E | 4.1457 E | 4.1458 E | 4.1459 E | 4.1460 E | 4.1461 E | 4.1462 E | 4.1463 E | 4.1464 E | 4.1465 E | 4.1466 E | 4.1467 E | 4.1468 E | 4.1469 E | 4.1470 E | 4.1471 E | 4.1472 E | 4.1473 E | 4.1474 E | 4.1475 E | 4.1476 E | 4.1477 E | 4.1478 E | 4.1479 E | 4.1480 E | 4.1481 E | 4.1482 E | 4.1483 E | 4.1484 E | 4.1485 E | 4.1486 E | 4.1487 E | 4.1488 E | 4.1489 E | 4.1490 E | 4.1491 E | 4.1492 E | 4.1493 E | 4.1494 E | 4.1495 E | 4.1496 E | 4.1497 E | 4.1498 E | 4.1499 E | 4.1500 E | 4.1501 E | 4.1502 E | 4.1503 E | 4.1504 E | 4.1505 E | 4.1506 E | 4.1507 E | 4.1508 E | 4.1509 E | 4.1510 E | 4.1511 E | 4.1512 E | 4.1513 E | 4.1514 E | 4.1515 E | 4.1516 E | 4.1517 E | 4.1518 E | 4.1519 E | 4.1520 E | 4.1521 E | 4.1522 E | 4.1523 E | 4.1524 E | 4.1525 E | 4.1526 E | 4.1527 E | 4.1528 E | 4.1529 E | 4.1530 E | 4.1531 E | 4.1532 E | 4.1533 E | 4.1534 E | 4.1535 E | 4.1536 E | 4.1537 E | 4.1538 E | 4.1539 E | 4.1540 E | 4.1541 E | 4.1542 E | 4.1543 E | 4.1544 E | 4.1545 E | 4.1546 E | 4.1547 E | 4.1548 E | 4.1549 E | 4.1550 E | 4.1551 E | 4.1552 E | 4.1553 E | 4.1554 E | 4.1555 E | 4.1556 E | 4.1557 E | 4.1558 E | 4.1559 E | 4.1560 E | 4.1561 E | 4.1562 E | 4.1563 E | 4.1564 E | 4.1565 E | 4.1566 E | 4.1567 E | 4.1568 E | 4.1569 E | 4.1570 E | 4.1571 E | 4.1572 E | 4.1573 E | 4.1574 E | 4.1575 E | 4.1576 E | 4.1577 E | 4.1578 E | 4.1579 E | 4.1580 E | 4.1581 E | 4.1582 E | 4.1583 E | 4.1584 E | 4.1585 E | 4.1586 E | 4.1587 E | 4.1588 E | 4.1589 E | 4.1590 E | 4.1591 E | 4.1592 E | 4.1593 E | 4.1594 E | 4.1595 E | 4.1596 E | 4.1597 E | 4.1598 E | 4.1599 E | 4.1600 E | 4.1601 E | 4.1602 E | 4.1603 E | 4.1604 E | 4.1605 E | 4.1606 E | 4.1607 E | 4.1608 E | 4.1609 E | 4.1610 E | 4.1611 E | 4.1612 E | 4.1613 E | 4.1614 E | 4.1615 E | 4.1616 E | 4.1617 E | 4.1618 E | 4.1619 E | 4.1620 E | 4.1621 E | 4.1622 E | 4.1623 E | 4.1624 E | 4.1625 E | 4.1626 E | 4.1627 E | 4.1628 E | 4.1629 E | 4.1630 E | 4.1631 E | 4.1632 E | 4.1633 E | 4.1634 E | 4.1635 E | 4.1636 E | 4.1637 E | 4.1638 E | 4.1639 E | 4.1640 E | 4.1641 E | 4.1642 E | 4.1643 E | 4.1644 E | 4.1645 E | 4.1646 E | 4.1647 E | 4.1648 E | 4.1649 E | 4.1650 E | 4.1651 E | 4.1652 E | 4.1653 E | 4.1654 E | 4.1655 E | 4.1656 E | 4.1657 E | 4.1658 E | 4.1659 E | 4.1660 E | 4.1661 E | 4.1662 E | 4.1663 E | 4.1664 E | 4.1665 E | 4.1666 E | 4.1667 E | 4.1668 E | 4.1669 E | 4.1670 E | 4.1671 E | 4.1672 E | 4.1673 E | 4.1674 E | 4.1675 E | 4.1676 E | 4.1677 E | 4.1678 E | 4.1679 E | 4.1680 E | 4.1681 E | 4.1682 E | 4.1683 E | 4.1684 E | 4.1685 E | 4.1686 E | 4.1687 E | 4.1688 E | 4.1689 E | 4.1690 E | 4.1691 E | 4.1692 E | 4.1693 E | 4.1694 E | 4.1695 E | 4.1696 E | 4.1697 E | 4.1698 E | 4.1699 E | 4.1700 E | 4.1701 E | 4.1702 E | 4.1703 E | 4.1704 E | 4.1705 E | 4.1706 E | 4.1707 E | 4.1708 E | 4.1709 E | 4.1710 E | 4.1711 E | 4.1712 E | 4.1713 E | 4.1714 E | 4.1715 E | 4.1716 E | 4.1717 E | 4.1718 E | 4.1719 E | 4.1720 E | 4.1721 E | 4.1722 E | 4.1723 E | 4.1724 E | 4.1725 E | 4.1726 E | 4.1727 E | 4.1728 E | 4.1729 E | 4.1730 E | 4.1731 E | 4.1732 E | 4.1733 E | 4.1734 E | 4.1735 E | 4.1736 E | 4.1737 E | 4.1738 E | 4.1739 E | 4.1740 E | 4.1741 E | 4.1742 E | 4.1743 E | 4.1744 E | 4.1745 E | 4.1746 E | 4.1747 E | 4.1748 E | 4.1749 E | 4.1750 E | 4.1751 E | 4.1752 E | 4.1753 E | 4.1754 E | 4.1755 E | 4.1756 E | 4.1757 E | 4.1758 E | 4.1759 E | |
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| S0116: 1, H0341: 1, H0661: 1, H0177: 1, H0306: 1, S0418: 1, S0356: 1, H0208: 1, S0046: 1, H0645: 1, H0393: 1, S0300: 1, L0717: 1, S6014: 1, H0438: 1, H0586: 1, H0333: 1, H0331: 1, H0632: 1, L0622: 1, H0486: 1, T0040: 1, L0586: 1, T0060: 1, H0244: 1, H0599: 1, H0098: 1, H0590: 1, H0004: 1, H0581: 1, H0421: 1, S0049: 1, H0196: 1, L2250: 1, H0235: 1, H0596: 1, T0115: 1, T0110: 1, H0597: 1, H0546: 1, H0545: 1, H0150: 1, H0009: 1, H0178: 1, H0123: 1, L0471: 1, H0012: 1, H0014: 1, H0015: 1, H0373: 1, S0388: 1, T0010: 1, | |
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Table 3.3.3.3

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| 319 | HFAAJ44 | 646715 744764 489201 | 616 617 329 | 151 - 20 39 - 221 3 - 299 | 1229 1230 942 | Cys-11 to His-18. | L0606: 1, L0657: 1, L0493: 1, L0518: 1, L0782: 1, L0545: 1, L0529: 1, L0647: 1, L0792: 1, L0532: 1, S0148: 1, H0547: 1, H0593: 1, H0365: 1, H0689: 1, H0682: 1, H0684: 1, H0435: 1, H0670: 1, H0666: 1, S0380: 1, L0602: 1, S0152: 1, S0013: 1, S0146: 1, H0555: 1, H0478: 1, H0540: 1, S3012: 1, S0037: 1, S0206: 1, L0756: 1, L0777: 1, H0444: 1, H0595: 1, L0589: 1, S0011: 1, H0668: 1, H0665: 1, H0667: 1, S0194: 1, S0276: 1, H0542: 1, S0384: 1, H0506: 1 and H0352: 1. | | |
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| 320 | HSLEM44 | 506604 | 330 | 2 - 349 | 943 | Gln-1 to Gly-11. | S6024: 1 and S0196: 1. AR061: 1, AR089: 0 T0074: 1 and S0028: 1. | | |
| 321 | HETCL79 | 522826 | 331 | 478 - 152 | 944 | | AR089: 7, AR061: 6 H0046: 2, L0744: 2, H0581: 1 and H0547: 1. | 1q21 | 104770, 107670, 110700, 135940, 145001, 146790, 152445, 152445, 159001, 174000, 179755, 182860, 182860, 182860, 191315, 230800, 230800, 266200, 600897, 601105, 601412, 601652, 602491 |

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| 322 | HFTAR20 | 670041 | 332 | 3 - 443 | 945 | | AR089: 6, AR061: 4 L0749: 6, L0794: 4, H0123: 1, L0768: 1 and S0194: 1. | | |
| 323 | HCUFD32 | 699379 | 333 | 1 - 498 | 946 | Thr-1 to Leu-11, Lys-24 to Ile-29, Gln-134 to Asn-144, Gln-150 to Thr-165. | AR089: 7, AR061: 3 L0754: 6, L0439: 2, L0751: 2, L0747: 2, H0661: 1, H0402: 1, H0272: 1, L0438: 1, H0696: 1 and L0779: 1. | | |
| 324 | HKAEO39 | 705332 | 334 | 2 - 463 | 947 | Lys-20 to Ser-28, Arg-44 to Ala-52, Leu-83 to Glu-89. | AR089: 0, AR061: 0 L0792: 2, S0420: 1, H0645: 1, H0494: 1, L0806: 1, L0807: 1, L0740: 1 and L0752: 1. | | |
| 325 | HLWBR95 | 734474 | 335 | 3 - 476 | 948 | | AR089: 3, AR061: 1 S0420: 1, H0550: 1, H0587: 1, H0485: 1, H0150: 1, H0553: 1, T0042: 1, L0530: 1 and S0152: 1. | 10q23 174900, 236730, 601493 | |
| 326 | HPWCJ63 | 772553 | 336 | 148 - 807 | 949 | Lys-213 to Gly-220. | AR054: 2, AR051: 1, AR061: 0, AR089: 0, AR050: 0 S0001: 1, H0191: 1 and S0044: 1. | | |

| | | 957495 | 618 | 1239 - 580 | 1231 | Lys-213 to Gly-220. | | | |
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| 327 | HBXCM35 | 782911 | 337 | 592 - 98 | 950 | | AR089: 8, AR061: 4 L0743: 2, S0040: 1, H0663: 1, H0427: 1, H0545: 1, S0250: 1, H0087: 1, S0038: 1, L0804: 1 and L0783: 1. | | |
| 328 | HULBN83 | 857836 | 338 | 1 - 636 | 951 | | AR089: 1, AR061: 1 H0619: 2, L0779: 2, S0222: 1, H0530: 1, H0433: 1, L0766: 1 and L0753: 1. | | |
| 329 | HAGET77 | 885265 | 339 | 86 - 850 | 952 | Lys-26 to Gln-36, Leu-50 to Glu-56, Gly-93 to Thr-106, Gln-108 to Gly-122, Gly-132 to Gln-138, Ser-144 to Trp-153, Glu-155 to Glu-171, Lys-178 to Pro-198, Val-207 to Asn-230, Arg-235 to Asp-247. | AR061: 4, AR089: 2 S0010: 3, S0036: 3, L0766: 3, S0222: 2, S0346: 2, H0310: 2, H0327: 2, H0457: 2, H0656: 1, S0282: 1, S6016: 1, S0665: 1, L2250: 1, H0051: 1, S0386: 1, H0342: 1, S0031: 1, L0366: 1 and H0543: 1. | | |
| 330 | HMSOZ55 | 910911 | 340 | 3 - 503 | 953 | Lys-22 to Gly-27. | AR089: 6, AR061: 3 S0282: 1, T0040: 1, H0013: 1, S0182: 1, | | |

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| 331 | HAPOR42 | 911292 | 341 | 6 - 701 | 954 | | | S0426: 1, H0670: 1, H0667: 1 and H0542: 1. | | |
| 332 | HMVAU10 | 911449 | 342 | 2 - 538 | 955 | | | AR089: 21, AR061: 10 H0156: 1, H0575: 1, H0590: 1, H0263: 1 and L0362: 1. | | |
| 333 | HTTFY29 | 911454 | 343 | 3 - 644 | 956 | | Arg-37 to Arg-44, Asn-47 to Glu-56, Lys-65 to Glu-70, Arg-78 to Pro-83, Gln-98 to Asp-106, Pro-142 to Ile-151, Ala-154 to Thr-180. | AR054: 16, AR051: 13, AR061: 8, AR089: 3, AR050: 1 H0040: 1, H0022: 1, S0152: 1 and H0521: 1. | | |
| 334 | HHFJY06 | 911456 | 344 | 81 - 584 | 957 | | Glu-11 to Ser-21, Asn-52 to Ser-57, Arg-81 to Met-88, Glu-139 to Tyr-146, Glu-153 to Leu-159. | AR089: 10, AR061: 6 H0619: 1, S0036: 1, H0135: 1 and H0520: 1. | | |
| 335 | HPCIK72 | 911459 | 345 | 283 - 2 | 958 | | | AR089: 1, AR061: 0 S0358: 1, H0642: 1 and H0264: 1. | | |
| 336 | HFIDT84 | 919878 | 346 | 64 - 2151 | 959 | | Asp-51 to His-60, Thr-105 to Pro-117, Asp-143 to Ala-151, | AR089: 9, AR061: 5 S0192: 2, S0222: 1, H0562: 1, H0373: 1 and | | |

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| 337 | HMC/V88 | 924874 | 347 | 40 - 516 | 960 | <p>Asp-167 to Ile-192, Ala-212 to Thr-223, Arg-325 to Asp-346, Lys-354 to Glu-359, Gln-390 to Asp-395, Arg-406 to Ser-412, Gln-431 to Asp-438, Ser-447 to Leu-465, Arg-516 to Thr-522, Lys-561 to Ser-570, Pro-583 to Pro-589, Tyr-625 to Asn-631, Pro-644 to Arg-650.</p> | S0242: 1. | | |
| | | | | | | <p>Glu-19 to Asp-28, Tyr-37 to Ala-42, Pro-53 to Leu-59, Ile-67 to Gly-74, Arg-152 to Val-158.</p> | <p>AR089: 11, AR061: 6 L0748: 10, L0751: 9, L0769: 7, L0779: 7, S0126: 5, S0022: 4, L0775: 4, L0740: 4, L0747: 4, L0752: 4, L0731: 4, L0596: 4, S0142: 3, L0771: 3, L0757: 3, L0599: 3, T0039: 2, H0013: 2, S0346: 2, S0003: 2, T0041: 2, S0344: 2, L0770: 2, L0773: 2.</p> | | |

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| | L0766: 2, L0776: 2, L0663: 2, L0565: 2, S0027: 2, L0742: 2, L0754: 2, L0750: 2, L0753: 2, L0759: 2, L0588: 2, L0362: 2, H0624: 1, L0002: 1, H0656: 1, S0212: 1, S0420: 1, S0356: 1, H0441: 1, L0034: 1, L0738: 1, H0546: 1, H0012: 1, H0620: 1, H0024: 1, H0014: 1, H0083: 1, H0622: 1, T0006: 1, H0617: 1, H0068: 1, H0090: 1, H0063: 1, H0334: 1, H0561: 1, S0150: 1, H0633: 1, L0372: 1, L0662: 1, L0804: 1, L0774: 1, L0656: 1, L0636: 1, L0635: 1, L0783: 1, L0384: 1, L0809: 1, L0528: 1, L0666: 1, L0664: 1, H0144: 1, H0547: 1, | | | | | | | | |
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| 338 | HKAIP73 | 928809 | 348 | 1455 - 487 | 961 | Ser-3 to Asp-8, Ser-39 to Pro-61, Ser-63 to Ser-69, > Lys-144 to Thr-150, Asp-187 to Gly-193. | AR089: 3, AR061: 2 H0031: 9, L0659: 7, S0358: 5, H0622: 5, H0494: 5, L0438: 4, L0743: 4, S0132: 3, H0040: 3, L0800: 3, L0771: 3, S0354: 2, H0014: 2, L0483: 2, L0764: 2, L0783: 2, L0587: 2, L0601: 2, S0114: 1, H0661: 1, S0356: 1, S0442: 1, S0360: 1, H0592: 1, H0587: 1, H0036: 1, H0590: 1, H0024: 1, H0510: 1, H0252: 1, H0039: 1, H0553: 1, S0440: 1, L0772: 1, | H0670: 1, H0648: 1, H0539: 1, S0152: 1, S0406: 1, H0540: 1, S3014: 1, L0745: 1, L0777: 1, L0755: 1, L0758: 1, H0445: 1, L0592: 1, H0667: 1, S0194: 1 and H0423: 1. | | |
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| | | | | | | | | L0646: 1, L0374: 1, L0773: 1, L0766: 1, L0803: 1, L0804: 1, L0774: 1, L0784: 1, L0806: 1, L0653: 1, L0655: 1, S0374: 1, S0328: 1, S3012: 1, L0749: 1, L0731: 1, L0758: 1 and H0677: 1. | | | |
| 339 | HFVHV40 | 945849 | 349 | 6 - 680 | 962 | Pro-8 to Arg-29, Tyr-156 to Asp-161, Glu-172 to Pro-184, Arg-194 to Asn-203. | | AR061: 5, AR089: 3 S0152: 3, H0619: 2, S6024: 1, H0341: 1, S0212: 1, H0393: 1, H0592: 1, H0575: 1, H0036: 1, H0052: 1, N0006: 1, H0083: 1, L0483: 1, H0100: 1, H0494: 1, S0144: 1, S0002: 1, H0703: 1, H0522: 1, H0134: 1, H0436: 1 and H0653: 1. | | | |
| 340 | HTJNI80 | 952231 | 350 | 2 - 598 | 963 | | | AR089: 10, AR061: 4 H0650: 2, S3014: 2, H0265: 1, H0581: 1, L0034: 1, H0488: 1, H0547: 1, H0518: 1. | | | |

| Parameter | Value | Unit | Parameter | Value | Unit |
|------------|-------|------|------------|-------|------|
| α | 0.001 | | β | 0.001 | |
| γ | 0.001 | | δ | 0.001 | |
| ϵ | 0.001 | | ζ | 0.001 | |
| η | 0.001 | | θ | 0.001 | |
| ι | 0.001 | | κ | 0.001 | |
| λ | 0.001 | | μ | 0.001 | |
| ν | 0.001 | | ξ | 0.001 | |
| \omicron | 0.001 | | π | 0.001 | |
| ρ | 0.001 | | σ | 0.001 | |
| τ | 0.001 | | υ | 0.001 | |
| ϕ | 0.001 | | χ | 0.001 | |
| ψ | 0.001 | | ω | 0.001 | |
| Ω | 0.001 | | Θ | 0.001 | |
| Φ | 0.001 | | Ψ | 0.001 | |
| Υ | 0.001 | | Ξ | 0.001 | |
| Λ | 0.001 | | Σ | 0.001 | |
| Π | 0.001 | | Υ | 0.001 | |
| Γ | 0.001 | | Δ | 0.001 | |
| Σ | 0.001 | | Θ | 0.001 | |
| Δ | 0.001 | | Λ | 0.001 | |
| Θ | 0.001 | | Ξ | 0.001 | |
| Λ | 0.001 | | Σ | 0.001 | |
| Ξ | 0.001 | | Υ | 0.001 | |
| Σ | 0.001 | | Δ | 0.001 | |
| Υ | 0.001 | | Θ | 0.001 | |
| Δ | 0.001 | | Λ | 0.001 | |
| Θ | 0.001 | | Ξ | 0.001 | |
| Λ | 0.001 | | Σ | 0.001 | |
| Ξ | 0.001 | | Υ | 0.001 | |
| Σ | 0.001 | | Δ | 0.001 | |
| Υ | 0.001 | | Θ | 0.001 | |
| Δ | 0.001 | | Λ | 0.001 | |
| Θ | 0.001 | | Ξ | 0.001 | |
| Λ | 0.001 | | Σ | 0.001 | |
| Ξ | 0.001 | | Υ | 0.001 | |
| Σ | 0.001 | | Δ | 0.001 | |
| Υ | 0.001 | | Θ | 0.001 | |
| Δ | 0.001 | | Λ | 0.001 | |
| Θ | 0.001 | | Ξ | 0.001 | |
| Λ | 0.001 | | Σ | 0.001 | |
| Ξ | 0.001 | | Υ | 0.001 | |
| Σ | 0.001 | | Δ | 0.001 | |
| Υ | 0.001 | | Θ | 0.001 | |
| Δ | 0.001 | | Λ | 0.001 | |
| Θ | 0.001 | | Ξ | 0.001 | |
| Λ | 0.001 | | Σ | 0.001 | |
| Ξ | 0.001 | | Υ | 0.001 | |
| Σ | 0.001 | | Δ | 0.001 | |
| Υ | 0.001 | | Θ | 0.001 | |
| Δ | 0.001 | | Λ | 0.001 | |
| Θ | 0.001 | | Ξ | 0.001 | |
| Λ | 0.001 | | Σ | 0.001 | |
| Ξ | 0.001 | | Υ | 0.001 | |
| Σ | 0.001 | | Δ | 0.001 | |
| Υ | 0.001 | | Θ | 0.001 | |
| Δ | 0.001 | | Λ | 0.001 | |
| Θ | 0.001 | | Ξ | 0.001 | |
| Λ | 0.001 | | Σ | 0.001 | |
| Ξ | 0.001 | | Υ | 0.001 | |
| Σ | 0.001 | | Δ | 0.001 | |
| Υ | 0.001 | | Θ | 0.001 | |
| Δ | 0.001 | | Λ | 0.001 | |
| Θ | 0.001 | | Ξ | 0.001 | |
| Λ | 0.001 | | Σ | 0.001 | |
| Ξ | 0.001 | | Υ | 0.001 | |
| Σ | 0.001 | | Δ | 0. | |

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|-----|---------|--------|-----|-----------|-----|--|--|--|--|
| 341 | HEAAE08 | 959970 | 351 | 133 - 621 | 964 | Pro-1 to Pro-12, Pro-53 to Gly-58, Gly-65 to Ser-71, Gly-106 to Lys-111, Lys-143 to Gly-163. | S0152: 1, S0260: 1 and L0366: 1. | | |
| | | | | | | | AR061: 10, AR089: 4 L0789: 6, L0809: 2, H0669: 1, H0369: 1, H0252: 1, L0055: 1, L0763: 1, L0770: 1, L0638: 1, L0803: 1, L0805: 1, L0776: 1, L0753: 1, L0758: 1, L0592: 1 and H0543: 1. | | |
| 342 | HDPLU91 | 963199 | 352 | 2 - 748 | 965 | Pro-53 to Val-58, Pro-85 to Ser-95, Gln-132 to Gly-138. | AR089: 16, AR061: 5 L0439: 10, L0526: 6, L0005: 5, L0740: 5, S0422: 4, L0438: 4, L0758: 4, L0581: 4, H0370: 3, H0486: 3, S0003: 3, H0144: 3, H0659: 3, H0672: 3, L0744: 3, L0754: 3, L0731: 3, L0595: 3, H0657: 2, H0664: 2, S0418: 2, S0376: 2, H0431: 2, H0050: 2, L0471: 2, H0083: 2, H0266: 2, H0090: 2. | | |

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|--|--|--|--|--|--|--|--|--|--|
| | | | | | H0616: 2, L0770: 2, L0769: 2, L0761: 2, L0766: 2, L0655: 2, L0657: 2, L0659: 2, L0783: 2, L0519: 2, L0666: 2, L0756: 2, L0759: 2, S0260: 2, H0595: 2, L0588: 2, L0589: 2, L0590: 2, L0608: 2, S0192: 2, H0265: 1, T0049: 1, H0650: 1, L0481: 1, H0638: 1, S0356: 1, T0008: 1, H0208: 1, S0045: 1, L0010: 1, H0611: 1, H0455: 1, H0574: 1, H0492: 1, H0635: 1, L0021: 1, H0575: 1, S0010: 1, H0318: 1, H0581: 1, H0052: 1, H0251: 1, H0597: 1, H0046: 1, L0157: 1, H0051: 1, S0048: 1, H0188: 1, L0483: 1, H0644: 1, L0455: 1, S0036: 1, | | | | |
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|-----|---------|--------|-----|---------|-----|--|---|---|--|
| 343 | HAPRM21 | 963200 | 353 | 1 - 630 | 966 | Gln-8 to Gly-14, Thr-164 to Gly-183, Pro-197 to Asp-210. | AR089: 25, AR061: 5 H0123: 2, L0754: 2, H0650: 1, H0550: 1, | AR089: 25, AR061: 5 H0123: 2, L0754: 2, H0650: 1, H0550: 1, | |
|-----|---------|--------|-----|---------|-----|--|---|---|--|

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|-----|---------|--------|-----|---------|-----|--|--|--|--|--|--|
| 344 | HTDAB30 | 965320 | 354 | 3 - 944 | 967 | | | | H0244: 1, H0427: 1, H0575: 1, S0010: 1 and L0698: 1. | | |
| | | | | | | | | | AR089: 5, AR061: 4 S0152: 7, L0748: 7, L0779: 6, L0766: 5, H0591: 4, L0771: 4, L0749: 4, L0777: 4, L0759: 4, H0556: 3, L0803: 3, L0783: 3, H0521: 3, L0754: 3, L0731: 3, L0595: 3, H0423: 3, H0170: 2, H0657: 2, H0341: 2, H0013: 2, H0598: 2, H0412: 2, H0494: 2, L0768: 2, L0526: 2, L0663: 2, S0328: 2, L0755: 2, L0757: 2, H0542: 2, S0420: 1, S0358: 1, S0408: 1, H0619: 1, H0587: 1, H0486: 1, T0060: 1, H0575: 1, H0036: 1, H0318: 1, H0581: 1, H0434: 1, H0544: 1, | | |

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|-----|---------|--------|-----|---------|-----|--|--|--|---|--|--|--|--|--|
| | | | | | | | | | H0014: 1, H0687: 1, H0644: 1, H0163: 1, H0090: 1, H0551: 1, H0477: 1, H0264: 1, H0268: 1, H0623: 1, H0560: 1, S0370: 1, S0002: 1, H0529: 1, L0520: 1, L0769: 1, L0774: 1, L0606: 1, L0807: 1, L0659: 1, L0384: 1, L0790: 1, L0664: 1, S0052: 1, H0702: 1, H0547: 1, H0519: 1, H0684: 1, H0518: 1, H0696: 1, S0432: 1, L0780: 1, L0752: 1, L0758: 1, L0596: 1, L0608: 1, H0667: 1, H0543: 1 and S0446: 1. | | | | | |
| 345 | H2CBN90 | 966919 | 355 | 3 - 821 | 968 | | | | AR061: 4, AR089: 4 L0794: 6, S0360: 3, T0110: 2, L0455: 2, L0649: 2, L0498: 2, L0659: 2, L0791: 2, L0748: 2, L0731: 2, | | | | | |

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| 347 | HADEX52 | 971351 | 357 | 38 - 1354 | 970 | Arg-11 to Arg-18, Glu-23 to Glu-28, Asn-40 to Leu-45, Thr-53 to Asp-58, Lys-74 to Asp-82, Val-92 to Glu-97, | S0418: 1, S0358: 1, S0376: 1, S0360: 1, S0132: 1, H0642: 1, H0590: 1, H0150: 1, H0620: 1, H0023: 1, H0356: 1, H0424: 1, H0213: 1, H0617: 1, H0169: 1, H0634: 1, H0063: 1, T0067: 1, H0488: 1, H0334: 1, S0370: 1, H0652: 1, L0645: 1, L0773: 1, L0648: 1, L0806: 1, L0776: 1, L0541: 1, L0789: 1, L0790: 1, L0664: 1, S0374: 1, H0689: 1, H0666: 1, H0672: 1, H0478: 1, L0748: 1, L0779: 1, S0436: 1 and H0506: 1. | | |
| 347 | HADEX52 | 971351 | 357 | 38 - 1354 | 970 | Arg-11 to Arg-18, Glu-23 to Glu-28, Asn-40 to Leu-45, Thr-53 to Asp-58, Lys-74 to Asp-82, Val-92 to Glu-97, | AR054: 40, AR050: 30, AR051: 28, AR089: 1, AR061: 1 S0270: 8, S0268: 7, L0731: 4, L0471: 3, H0201: 2, H0547: 2, | | |

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| | | | | | | Ser-104 to Asn-109, Asp-127 to Phe-133, Gln-158 to Asp-170, Asn-177 to Ala-207. | S0274: 2, L0754: 2, L0604: 2, S0202: 1, S0252: 1, S0360: 1, H0550: 1, H0600: 1, H0333: 1, H0486: 1, H0013: 1, H0427: 1, H0599: 1, H0575: 1, S0010: 1, H0194: 1, H0327: 1, H0569: 1, H0594: 1, S0628: 1, S0250: 1, H0622: 1, L0544: 1, H0144: 1, L0438: 1, H0519: 1, S0126: 1, L0744: 1, L0747: 1, L0777: 1, S0242: 1 and S0196: 1. | | |
| 348 | HTADZ74 | 811489 | 358 | 23 - 586 | 971 | Ile-5 to Lys-10, Arg-78 to Asp-92. | AR050: 18, AR089: 2, AR061: 2, AR051: 2, AR054: 1 S0114: 1, H0069: 1, H0014: 1, L0667: 1, L0804: 1, L0659: 1, S0052: 1 and H0422: 1. | | |
| 349 | HAPNZ77 | 887072 | 359 | 1 - 483 | 972 | Lys-82 to Gln-87, Asp-103 to Ala-108, Glu-122 to Lys-127. | AR089: 70, AR061: 14, AR050: 9, AR051: 1, AR054: 1 | | |

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| 350 | HELDR74 | 963001 | 360 | 3 - 1223 | 973 | His-14 to Gln-19. | L0766: 2, H0575: 1, H0264: 1, L0761: 1 and L0804: 1. | | |
| | | | | | | | AR089: 1, AR061: 0 H0305: 4, L0731: 3, L0581: 3, H0622: 2, H0059: 2, L0764: 2, L0766: 2, L0741: 2, L0740: 2, L0749: 2, H0423: 2, H0149: 1, H0159: 1, S0114: 1, H0656: 1, H0255: 1, H0306: 1, H0402: 1, S0045: 1, H0351: 1, H0550: 1, H0441: 1, H0036: 1, T0048: 1, H0318: 1, H0581: 1, H0024: 1, H0051: 1, H0083: 1, H0510: 1, H0617: 1, H0412: 1, H0280: 1, H0647: 1, L0646: 1, L0374: 1, L0385: 1, L0662: 1, L0767: 1, L0794: 1, L0649: 1, L0774: 1, L0806: 1, L0653: 1, | | |

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| 351 | HDPLJ22 | 859915 | 361 | 2 - 547 | 974 | Phe-20 to Lys-37, Asn-108 to Arg-116. | L0657: 1, L0659: 1, L0783: 1, S0126: 1, H0690: 1, H0670: 1, H0672: 1, S0328: 1, S0380: 1, H0555: 1, L0748: 1, L0752: 1, L0758: 1, S0194: 1, H0542: 1 and H0422: 1. AR089: 1, AR061: 0 L0591: 20, L0748: 13, H0090: 5, H0521: 4, L0758: 4, H0556: 3, H0656: 3, S0358: 3, H0038: 3, S0002: 3, L0794: 3, L0766: 3, L0803: 3, L0805: 3, L0791: 3, L0665: 3, H0547: 3, S0328: 3, L0747: 3, H0423: 3, H0624: 2, S0420: 2, S0046: 2, H0427: 2, H0156: 2, H0046: 2, L0471: 2, H0510: 2, H0424: 2, H0181: 2, H0264: 2, H0100: 2, S0426: 2, L0631: 2. | | |
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| | | | | | H0539: 2, S0380: 2, S0152: 2, H0555: 2, S3014: 2, S0206: 2, L0777: 2, L0731: 2, H0422: 2, H0686: 1, L0002: 1, H0657: 1, H0663: 1, H0662: 1, S0348: 1, S0360: 1, S0007: 1, S0278: 1, H0600: 1, H0497: 1, H0559: 1, T0039: 1, H0013: 1, H0599: 1, H0575: 1, H0004: 1, H0318: 1, H0581: 1, H0421: 1, H0263: 1, H0050: 1, H0082: 1, H0373: 1, H0071: 1, H0629: 1, S0003: 1, H0328: 1, H0031: 1, H0553: 1, H0111: 1, H0628: 1, H0617: 1, H0673: 1, S0364: 1, H0135: 1, H0163: 1, T0067: 1, H0561: 1, S0440: 1, S0344: 1, L0761: 1, L0764: 1. |
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| 352 | HPMLD11 | 890204 | 362 | 562 - 2 | 975 | Gln-11 to Trp-22, Arg-27 to Gly-32, Pro-47 to Gly-53. | L0771: 1, L0773: 1, L0650: 1, L0776: 1, L0655: 1, L0606: 1, L0629: 1, L0659: 1, L0809: 1, L0792: 1, L0666: 1, H0520: 1, H0593: 1, H0689: 1, H0659: 1, S0330: 1, H0522: 1, H0627: 1, L0742: 1, L0439: 1, L0740: 1, L0749: 1, L0779: 1, L0752: 1, L0757: 1, L0759: 1, H0445: 1, L0485: 1, H0653: 1, S0196: 1, H0542: 1 and H0506: 1. | | |
| 352 | HPMLD11 | 890204 | 362 | 562 - 2 | 975 | Gln-11 to Trp-22, Arg-27 to Gly-32, Pro-47 to Gly-53. | AR054: 115, AR050: 108, AR051: 87, AR061: 4, AR089: 2 H0644: 3, S0408: 1, S0280: 1, H0620: 1, S0364: 1, L0637: 1, L0764: 1, S0044: 1, L0611: 1, L0777: 1, L0755: 1, L0731: 1 and S0194: 1. | | |

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| 353 | HMVDZ78 | 938574 | 363 | 2 - 250 | 976 | AR089: 2, AR061: 2 L0659: 8, L0666: 8, L0751: 7, L0665: 6, L0528: 5, L0743: 5, L0663: 4, H0052: 3, L0638: 3, L0646: 3, L0764: 3, L0662: 3, L0774: 3, L0747: 3, H0668: 3, S0192: 3, H0150: 2, H0620: 2, H0413: 2, H0649: 2, S0426: 2, L0763: 2, L0769: 2, L0648: 2, L0766: 2, L0653: 2, L0657: 2, S0126: 2, H0670: 2, L0754: 2, L0749: 2, H0685: 1, S0040: 1, H0650: 1, S0212: 1, H0255: 1, S0420: 1, S0045: 1, H0261: 1, H0391: 1, L0022: 1, H0581: 1, H0597: 1, H0544: 1, H0545: 1, H0123: 1, H0012: 1, H0024: 1, H0188: 1, S0250: 1, | | |
|-----|---------|--------|-----|---------|-----|---|--|--|

| α | β | γ | δ | ϵ | ζ | η | θ | ι | κ | λ | μ | ν | ξ | \omicron | π | ρ | σ | τ | υ | ϕ | χ | ψ | ω |
|----------|----------|----------|----------|------------|----------|----------|----------|----------|----------|-----------|----------|----------|----------|------------|----------|----------|----------|----------|------------|----------|----------|----------|----------|
| 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 |

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| | | | | | | | | | L0483: 1, H0617: 1, H0551: 1, H0494: 1, S0210: 1, L0372: 1, L0643: 1, L0773: 1, L0803: 1, L0650: 1, L0775: 1, L0375: 1, L0651: 1, L0525: 1, L0776: 1, L0661: 1, L0629: 1, L0664: 1, S0053: 1, L0565: 1, H0690: 1, H0682: 1, H0658: 1, H0648: 1, H0672: 1, H0539: 1, H0521: 1, S0044: 1, S0188: 1, H0555: 1, S3012: 1, L0752: 1, L0753: 1, L0757: 1, L0758: 1, L0592: 1, L0601: 1, L0603: 1 and H0352: 1. | | | | |
| 354 | HTSFJ40 | 956924 | 619 | 425 - 126 | 1232 | Gln-56 to Pro-70, Gly-78 to Gly-87. Leu-7 to Ala-13. | AR089: 30, AR061: 6 H0081: 1, H0087: 1, S0144: 1 and H0538: 1. | | | | | | |
| 355 | HEMBZ62 | 742551 | 365 | 2 - 454 | 978 | | AR089: 6, AR061: 2 | | | | | | |

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| 356 | HHFGZ38 | 785591 | 366 | 302 - 1165 | 979 | | | H0663: 2, S0328: 2, S0420: 1, S0046: 1, H0559: 1, T0082: 1, H0050: 1, H0100: 1, H0494: 1, L0640: 1, L0789: 1, H0436: 1 and L0439: 1. | | |
| 357 | HDPLN70 | 854010 | 367 | 40 - 828 | 980 | Pro-1 to Gly-7, Arg-15 to Trp-21, Pro-58 to Asn-63, Arg-82 to Gly-88. | | AR089: 8, AR061: 2 H0556: 1, S0040: 1, H0657: 1, H0306: 1, H0393: 1, H0050: 1, H0266: 1, H0112: 1, H0063: 1, S0142: 1, S0002: 1, L0794: 1, L0378: 1, L0655: 1, L0791: 1, L0665: 1, H0539: 1, H0521: 1, L0596: 1, L0593: 1, L0595: 1 and H0653: 1. | | |
| | | | | | | | | AR089: 2, AR061: 1 L0766: 26, L0439: 11, L0757: 8, H0521: 5, L0748: 5, H0462: 4, L0745: 4, L0777: 4, H0013: 3, H0123: 3, L0774: 3, H0522: 3, | | |

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| | | | | | | L0752: 3, S0356: 2, H0261: 2, S0222: 2, H0431: 2, H0427: 2, H0052: 2, H0545: 2, L0770: 2, L0769: 2, L0768: 2, L0806: 2, L0659: 2, H0144: 2, L0751: 2, L0756: 2, L0779: 2, L0591: 2, L0593: 2, H0667: 2, H0677: 2, H0656: 1, H0661: 1, S0358: 1, H0580: 1, S0045: 1, H0370: 1, H0486: 1, H0546: 1, S0022: 1, S0214: 1, H0328: 1, H0615: 1, H0428: 1, T0023: 1, H0628: 1, L0055: 1, H0032: 1, H0090: 1, H0059: 1, H0100: 1, L0351: 1, S0144: 1, S0002: 1, L0598: 1, L0764: 1, L0771: 1, L0662: 1, L0794: 1, L0775: 1, L0805: 1, L0545: 1, | | | | |
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| | | | | | | | | | L0543: 1, L0789: 1, L0790: 1, L0791: 1, L0792: 1, L0663: 1, H0520: 1, H0547: 1, H0519: 1, H0648: 1, L0740: 1, L0746: 1, L0747: 1, L0750: 1, L0759: 1, L0608: 1, L0601: 1, S0026: 1, H0665: 1, H0136: 1 and S0242: 1. | | | |
| 358 | HSDIH12 | 876344 | 368 | 3 - 623 | 981 | Thr-1 to Asp-19, Cys-23 to Cys-34, Gln-36 to Gln-58, Leu-78 to Gly-87, Asp-164 to His-169. | | | AR089: 24, AR061: 6 S0134: 1, L0749: 1, L0759: 1, S0260: 1 and L0596: 1. | | | |
| 359 | HNBUT01 | 913838 | 369 | 3 - 827 | 982 | Arg-1 to Gly-10. | | | AR089: 15, AR061: 5 S0360: 2, L0766: 2, L0747: 2, T0002: 1, H0686: 1, H0662: 1, S0046: 1, H0023: 1, H0560: 1, H0647: 1, L0662: 1, L0666: 1, H0576: 1, L0779: 1, L0596: 1, L0590: 1, L0601: 1 and H0667: 1. | | | |

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| 360 | HEOQN14 | 923752 | 370 | 1044 - 520 | 983 | | AR089: 15, AR061: 7 | | |
| 361 | HTXKL86 | 928194 | 371 | 1 - 762 | 984 | | AR061: 1, AR089: 1 L0438: 12, L0439: 11, H0617: 5, H0556: 4, H0618: 3, H0253: 3, L0769: 3, L0761: 3, L0759: 3, H0544: 2, H0031: 2, H0135: 2, H0038: 2, H0641: 2, L0764: 2, L0783: 2, L0809: 2, L0790: 2, L0666: 2, L0663: 2, L0665: 2, H0144: 2, S0330: 2, L0751: 2, L0779: 2, H0543: 2, H0265: 1, H0685: 1, H0657: 1, H0306: 1, S0420: 1, S0354: 1, S0360: 1, S0046: 1, L0717: 1, H0550: 1, H0592: 1, H0333: 1, H0331: 1, H0559: 1, H0486: 1, H0013: 1, H0244: 1, H0635: 1, H0575: 1, H0596: 1, | | |

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| 362 | HDQGV77 | 937546 | 372 | 12 - 1379 | 985 | Gln-24 to Gly-30, Asp-57 to Lys-62, Leu-109 to Thr-115, Asn-153 to Gln-166, Gly-168 to Glu-173, Gln-184 to Ala-199, Gly-221 to Pro-232, Pro-234 to Pro-243, | <p>T0110: 1, H0123: 1, H0615: 1, H0033: 1, H0553: 1, H0212: 1, H0124: 1, H0040: 1, H0616: 1, H0264: 1, H0488: 1, H0100: 1, H0494: 1, H0131: 1, H0529: 1, L0637: 1, L0772: 1, L0766: 1, L0775: 1, L0375: 1, L0776: 1, L0628: 1, L0657: 1, L0664: 1, S0374: 1, H0547: 1, H0593: 1, S3014: 1, S0027: 1, L0748: 1, L0750: 1, L0731: 1, L0758: 1, H0595: 1, S0276: 1 and H0423: 1.</p> <p>AR089: 4, AR061: 2 H0521: 17, S0007: 11, L0747: 11, H0543: 8, S0278: 7, H0581: 7, S0344: 7, L0766: 7, L0745: 7, H0556: 6, L0769: 6, L0748: 6, L0731: 6, L0601: 6,</p> | | |
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| | | | Gln-251 to Ser-259, Arg-273 to Gly-302, Lys-317 to Thr-349, Ala-351 to Arg-368. | H0584: 5, L0157: 5, H0424: 5, L0758: 5, H0542: 5, S0049: 4, H0150: 4, H0050: 4, H0135: 4, L0666: 4, H0522: 4, H0436: 4, L0439: 4, L0750: 4, H0423: 4, T0002: 3, H0656: 3, S0001: 3, H0619: 3, H0617: 3, T0042: 3, S0142: 3, S0002: 3, L0770: 3, L0761: 3, L0378: 3, L0659: 3, L0665: 3, H0422: 3, H0171: 2, H0650: 2, L0005: 2, H0645: 2, H0455: 2, H0156: 2, H0575: 2, H0309: 2, H0457: 2, H0178: 2, H0620: 2, T0010: 2, H0083: 2, S6028: 2, T0006: 2, H0604: 2, H0180: 2, H0598: 2, H0090: 2, H0264: 2, L0775: 2, L0375: 2, L0655: 2, | |
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| | | | | | L0635: 2, L0663: 2, H0697: 2, H0658: 2, S0027: 2, L0740: 2, L0756: 2, L0759: 2, H0445: 2, L0589: 2, L0599: 2, H0170: 1, H0265: 1, H0295: 1, H0583: 1, H0341: 1, H0255: 1, H0459: 1, H0638: 1, H0637: 1, S0045: 1, S6026: 1, H0351: 1, S6016: 1, S0222: 1, H0392: 1, H0574: 1, H0486: 1, H0013: 1, H0250: 1, H0069: 1, H0075: 1, H0427: 1, H0042: 1, H0036: 1, H0004: 1, S0010: 1, T0048: 1, H0318: 1, H0434: 1, H0052: 1, H0086: 1, H0572: 1, H0123: 1, H0012: 1, H0024: 1, S0051: 1, H0594: 1, H0428: 1, H0031: 1, H0165: 1, L0456: 1, |
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| 363 | HE8TM80 | 955022 | 373 | 358 - 696 | 986 | Arg-1 to Asn-7, Leu-56 to Met-61. | AR089: 9, AR061: 7 H0040: 5, H0547: 5, S0152: 5, L0593: 5, L0595: 5, H0551: 4, H0529: 4, H0519: 4, H0560: 3, H0561: 3, H0657: 2, S0360: 2, S0007: 2, H0586: 2, H0013: 2, H0494: 2, L0809: 2, H0435: 2, S0028: 2, L0748: 2, L0439: 2, L0731: 2, L0759: 2, H0445: 2, L0592: 2, H0542: 2, H0624: 1, H0170: 1, H0556: 1, S0212: 1, H0663: 1, S0418: 1, S0356: 1, S0046: 1, H0393: 1, H0486: 1, H0427: 1, H0156: 1, H0036: 1, H0318: 1, T0110: 1, H0545: 1, H0014: 1, H0266: 1, H0188: 1, S0022: 1, H0328: 1, H0688: 1, T0023: 1, H0032: 1, | | |
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| 364 | HWLEY40 | 957875 | 374 | 3 - 881 | 987 | Glu-6 to Gly-11, Gly-64 to Ser-70, Val-140 to Val-145, His-163 to Leu-168, Leu-189 to Lys-198, Ser-221 to Thr-227, His-261 to Pro-270. | AR089: 2, AR061: 2, L0438: 12, L0439: 11, H0617: 5, H0556: 4, H0618: 3, H0253: 3, L0769: 3, L0761: 3, L0759: 3, H0544: 2, H0031: 2, H0135: 2, H0038: 2, H0641: 2, L0764: 2, L0783: 2 | | | | | |

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| L0809: 2, L0790: 2, L0666: 2, L0663: 2, L0665: 2, H0144: 2, S0330: 2, L0751: 2, L0779: 2, H0543: 2, H0265: 1, H0685: 1, H0657: 1, H0306: 1, S0420: 1, S0354: 1, S0360: 1, S0046: 1, L0717: 1, H0550: 1, H0592: 1, H0333: 1, H0331: 1, H0559: 1, H0486: 1, H0013: 1, H0244: 1, H0635: 1, H0575: 1, H0596: 1, T0110: 1, H0123: 1, H0615: 1, H0033: 1, H0553: 1, H0212: 1, H0124: 1, H0040: 1, H0616: 1, H0264: 1, H0488: 1, H0100: 1, H0494: 1, H0131: 1, H0529: 1, L0637: 1, L0772: 1, L0766: 1, L0775: 1, L0375: 1, L0776: 1, L0628: 1, | | | | | | | | |
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| 365 | HDPDPD36 | 493820 | 375 | 403 - 272 | 988 | Trp-22 to Glu-35. | | | AR089: 1, AR061: 0 H0522: 2, L0439: 2, L0777: 2, H0591: 1, H0144: 1, H0521: 1, L0758: 1 and L0605: 1. | | | |
| | | 964320 | 620 | 2 - 436 | 1233 | Met-1 to Tyr-14, Arg-24 to Gly-30, His-49 to Cys-55, Ile-94 to Phe-99, Pro-128 to Gly-136. | | | | | | |
| 366 | HOUHZ94 | 527876 | 376 | 1 - 153 | 989 | Glu-1 to Thr-6. | | | AR061: 7, AR089: 3 H0161: 1 and S0040: 1. | 19p13.3 | | 108725, 120700, 133171, 136836, 145981, 147141, 164953, 188070, 600957. |

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| 367 | HMIAH32 | 550977 | 377 | 49 - 702 | 990 | His-15 to Ser-21, Asp-44 to Val-65, Glu-95 to Thr-101, Ala-131 to Asp-142. | AR061: 7, AR089: 2 S6028: 2, L0766: 2, L0777: 2, L0752: 2, H0663: 1, H0696: 1 and L0779: 1. | AR061: 7, AR089: 2 S6028: 2, L0766: 2, L0777: 2, L0752: 2, H0663: 1, H0696: 1 and L0779: 1. | 601238, 601846, 602216, 602477 |
| 368 | HDP4H43 | 573418 | 378 | 1 - 432 | 991 | Ser-28 to Glu-34, Ser-77 to Arg-82, Trp-127 to Arg-135. | AR061: 2, AR089: 1 S0116: 2, H0586: 1 and H0521: 1. | AR061: 2, AR089: 1 S0116: 2, H0586: 1 and H0521: 1. | |
| 369 | HCE3W04 | 615501 | 379 | 94 - 873 | 992 | | AR089: 1, AR061: 0 L0789: 4, L0731: 4, H0539: 3, L0779: 3, S0007: 2, H0052: 2, L0157: 2, H0123: 2, H0233: 2, L0637: 2, S0356: 1, S0360: 1, H0550: 1, H0253: 1, H0620: 1, H0408: 1, H0188: 1, S0250: 1, L0193: 1, L0455: 1, H0135: 1, H0551: 1, L0770: 1, L0794: 1, L0776: 1, L0665: 1, | AR089: 1, AR061: 0 L0789: 4, L0731: 4, H0539: 3, L0779: 3, S0007: 2, H0052: 2, L0157: 2, H0123: 2, H0233: 2, L0637: 2, S0356: 1, S0360: 1, H0550: 1, H0253: 1, H0620: 1, H0408: 1, H0188: 1, S0250: 1, L0193: 1, L0455: 1, H0135: 1, H0551: 1, L0770: 1, L0794: 1, L0776: 1, L0665: 1, | |

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| | | | | | | | | | L0779: 1, H0445: 1 and L0595: 1. | | | |
| 374 | HOQBF64 | 703177 | 384 | 48 - 401 | 997 | | | | AR089: 23, AR061: 14 H0208: 1 and H0290: 1. | 17q23-q24 | 106180, 115660, 138700, 139250, 148500, 150200, 154275, 162100, 170500, 170500, 170500, 176960, 182452, 230200, 249000, 253250 | |
| 375 | HTEDL38 | 761609 | 385 | 133 - 534 | 998 | Pro-38 to Pro-46. | | | AR061: 3, AR089: 2 H0038: 4, L0748: 4, S0222: 2, L0598: 2, L0776: 2, L0439: 2, L0780: 2, L0752: 2, H0050: 1, T0006: 1, H0111: 1, S0036: 1, H0616: 1, T0067: 1, | | | |

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| | | | | | | | | S0038: 1, L0770: 1, L0766: 1, L0774: 1, L0805: 1, L0655: 1, L0526: 1, L0666: 1, L0438: 1, S0028: 1, L0777: 1, L0595: 1 and L0366: 1. | | | |
| 376 | HE9HI71 | 779375 | 386 | 2 - 682 | 999 | | | AR089: 1, AR061: 1 H0013: 3, T0010: 1, L0435: 1, H0144: 1, L0438: 1 and L0439: 1. | | | |
| 377 | HNHFS82 | 779946 | 387 | 2 - 415 | 1000 | | | AR061: 4, AR089: 2 S0278: 1, H0620: 1 and H0271: 1. | | | |
| 378 | HOUHO89 | 786548 | 388 | 367 - 909 | 1001 | Ser-1 to Gly-7, Asp-24 to Leu-31, Lys-50 to Arg-58, Glu-65 to Arg-73, Thr-102 to His-109, Arg-116 to Ile-122. | | AR089: 1, AR061: 1 S0342: 1 and H0521: 1. | | | |
| 379 | HFPBB28 | 844526 | 389 | 3 - 335 | 1002 | Ala-11 to Gln-16, Leu-46 to Ala-52, Gln-84 to Glu-89, Phe-105 to Ser-111. | | AR054: 10, AR051: 2, AR050: 2, AR061: 1, AR089: 0 S0031: 2, S0001: 1, S0045: 1, S0222: 1, H0271: 1, S0144: 1, | | | |

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| 380 | HHEWQ61 | 876063 | 390 | 3 - 497 | 1003 | Thr-6 to Tyr-13, Ala-23 to Asp-30, Phe-66 to Arg-71, Pro-92 to Glu-102, Arg-108 to Leu-116, Tyr-159 to Thr-164. | L0368: 1, S0052: 1, S0146: 1, S0390: 1, S0028: 1 and S0260: 1. AR061: 1, AR089: 0 L0439: 4, H0543: 3, S0360: 2, L0662: 2, L0742: 2, L0481: 1, H0619: 1, H0486: 1, L0586: 1, L0021: 1, S0051: 1, H0424: 1, L0789: 1, S0374: 1, H0539: 1, L0744: 1, L0754: 1, L0777: 1, L0752: 1 and H0506: 1. | | |
| 381 | HUFGH09 | 877078 | 391 | 3 - 647 | 1004 | Leu-8 to Pro-14, Pro-59 to Asn-64, Pro-80 to Glu-91, Gly-127 to Lys-134, Arg-146 to Glu-152, Thr-156 to Asp-165, Pro-184 to Asp-203. | AR089: 3, AR061: 1 H0624: 2, S0356: 1, H0607: 1, L0060: 1 and H0506: 1. | | |
| 382 | HLICA79 | 880881 | 392 | 1 - 1197 | 1005 | Arg-1 to Gly-8, Gly-10 to Leu-17, Lys-41 to Pro-51, Lys-67 to Thr-74, Glu-94 to Lys-99, | AR051: 10, AR054: 10, AR050: 9, AR089: 5, AR061: 3 L0775: 4, H0046: 3, H0622: 3, H0660: 3, | | |

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| 383 | HSLIH01 | 884251 | 393 | 11 - 649 | 1006 | Phe-107 to Gly-112, Arg-125 to Glu-131, Leu-141 to Arg-153, Gly-168 to Ala-176, Asn-210 to Arg-215, Asn-222 to Ser-234, Leu-238 to Thr-249. | H0438: 2, L0663: 2, L0665: 2, L0777: 2, S0026: 2, H0583: 1, S0282: 1, S0356: 1, H0051: 1, H0071: 1, H0355: 1, H0510: 1, H0615: 1, H0428: 1, H0644: 1, L0142: 1, S0364: 1, H0059: 1, L0763: 1, L0803: 1, L0804: 1, L0657: 1, L0809: 1, L0664: 1, H0690: 1, H0670: 1, H0672: 1, H0479: 1, S0028: 1, L0751: 1, S0031: 1, L0604: 1, L0366: 1, S0192: 1 and S0424: 1. | | |
| | | | | | | Arg-14 to Glu-20, Leu-30 to Arg-42, Gly-57 to Ala-65, Asn-99 to Arg-104, Asn-111 to Ser-117. | AR089: 3, AR061: 2, AR051: 2, AR050: 1, AR054: 1 L0775: 4, H0046: 3, H0622: 3, H0660: 3, H0402: 2, H0438: 2, L0663: 2, L0665: 2, L0777: 2, S0026: 2, | | |

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| | | | | | | | | | H0583: 1, S0282: 1, S0356: 1, H0051: 1, H0071: 1, H0355: 1, H0510: 1, H0615: 1, H0428: 1, H0644: 1, L0142: 1, S0364: 1, H0059: 1, L0763: 1, L0803: 1, L0804: 1, L0657: 1, L0809: 1, L0666: 1, L0664: 1, H0144: 1, H0690: 1, H0670: 1, H0672: 1, H0479: 1, S0028: 1, L0751: 1, S0031: 1, L0604: 1, L0366: 1, S0192: 1 and S0424: 1. | | |
| 384 | HE9OV91 | 887364 | 394 | 34 - 723 | 1007 | | | | AR054: 2, AR051: 2, AR050: 1, AR089: 0, AR061: 0 S0116: 1, H0619: 1, H0421: 1, H0144: 1, L0748: 1 and L0758: 1. | | |
| 385 | HHEDS85 | 894602 | 395 | 2 - 457 | 1008 | Ser-12 to Ser-19, Ser-34 to Lys-47. | | | AR061: 2, AR089: 1 T0039: 1, H0144: 1 and H0542: 1. | | |
| 386 | HNTDJ68 | 899624 | 396 | 667 - 1599 | 1009 | Phe-40 to Tyr-47, | | | AR051: 25, AR050: | | |

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| 387 | HKAHO77 | 906671 | 397 | 712 - 398 | 1010 | Ile-119 to Arg-125, Ser-141 to Arg-200, Arg-217 to Lys-223, Ala-303 to Leu-311. | I3, AR089: 3, AR061: 2 L0731: 4, L0596: 4, H0615: 3, L0777: 3, H0625: 2, L0803: 2, L0740: 2, H0657: 1, H0393: 1, H0441: 1, T0109: 1, H0318: 1, H0581: 1, H0566: 1, H0551: 1, L0761: 1, L0641: 1, L0766: 1, L0650: 1, L0784: 1, H0144: 1, H0547: 1, H0539: 1, H0696: 1, S3014: 1, L0744: 1, L0779: 1 and L0780: 1. | | |
| 388 | HTFNP84 | 909687 | 398 | 70 - 1227 | 1011 | Tyr-11 to Val-16, | AR089: 19, AR061: 7 L0771: 4, L0764: 3, H0282: 2, H0494: 2, L0518: 2, L0617: 1, L0794: 1, L0774: 1, L0806: 1, L0657: 1, L0663: 1, S0374: 1, H0672: 1, L0752: 1 and L0755: 1. | | |

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| | | | Glu-37 to Arg-42, Asn-50 to Arg-58, Leu-82 to Leu-96, Glu-112 to Gln-120. | L0766: 15, L0646: 7, H0659: 5, L0749: 5, L0759: 5, S0374: 4, L0804: 3, H0547: 3, H0658: 3, H0170: 2, H0650: 2, S0418: 2, S0280: 2, H0598: 2, L0763: 2, L0803: 2, L0666: 2, L0663: 2, H0435: 2, H0660: 2, L0748: 2, L0757: 2, S0026: 2, S0424: 2, H0686: 1, H0657: 1, H0662: 1, S0420: 1, S0358: 1, S0376: 1, L0717: 1, H0574: 1, H0486: 1, H0596: 1, L0471: 1, H0024: 1, H0014: 1, H0083: 1, H0510: 1, H0266: 1, S0250: 1, S0003: 1, H0428: 1, H0032: 1, H0591: 1, H0040: 1, H0634: 1, H0616: 1, H0560: 1, S0440: 1, H0641: 1, H0529: 1, | | |
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| 389 | HDQGZ78 | 909735 | 399 | 5 - 442 | 1012 | Met-15 to Pro-20, Pro-47 to Arg-53, Tyr-61 to Asp-71. | AR061: 0, AR089: 0 H0521: 2, L0758: 2, H0038: 1, L0644: 1, L0645: 1, L0764: 1, L0662: 1, L0794: 1, L0557: 1, L0747: 1 and | | | L0520: 1, L0769: 1, L0761: 1, L0764: 1, L0521: 1, L0662: 1, L0774: 1, L0375: 1, L0805: 1, L0776: 1, L0655: 1, L0606: 1, L0659: 1, L0635: 1, L0367: 1, L0789: 1, L0665: 1, H0684: 1, H0670: 1, H0666: 1, H0672: 1, H0521: 1, H0704: 1, S0406: 1, L0439: 1, L0750: 1, L0756: 1, L0779: 1, L0777: 1, L0752: 1, L0755: 1, L0758: 1, L0608: 1, L0362: 1, H0667: 1, S0196: 1, H0543: 1, H0423: 1, H0422: 1 and H0352: 1. |
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| 390 | HHEMD52 | 909742 | 400 | 623 - 1618 | 1013 | Trp-3 to Thr-14, Ala-21 to Arg-30, Glu-66 to Pro-74, Pro-103 to Gly-108, Ile-135 to Ile-142. | L0779: 1. AR089: 4, AR061: 3 H0457: 3, H0271: 3, H0543: 3, H0422: 2, H0583: 1, H0650: 1, H0484: 1, H0483: 1, S0442: 1, H0580: 1, S0140: 1, H0486: 1, H0250: 1, H0050: 1, H0630: 1, H0264: 1, H0488: 1, H0487: 1, S0002: 1, L0439: 1, H0707: 1, H0136: 1 and H0677: 1. | | |
| 391 | HSIDQ38 | 909854 | 401 | 3 - 764 | 1014 | Ala-18 to Arg-23, Gly-28 to Trp-35, Gln-53 to Arg-61, Asp-122 to Glu-127, Gln-163 to Cys-171. | AR061: 3, AR089: 3 L0766: 5, H0587: 2, H0036: 2, L0745: 2, L0747: 2, H0556: 1, S0114: 1, H0590: 1, H0052: 1, L0640: 1, L0770: 1, L0771: 1, L0659: 1 and L0665: 1. | | |
| 392 | HSKBF02 | 909855 | 402 | 3 - 395 | 1015 | Gly-35 to Asp-41. | AR089: 53, AR061: 14 L0438: 6, L0751: 6, L0439: 5, L0770: 4, H0052: 2, H0620: 2, | | |

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| | | | | | | | | | H0521: 2, L0756: 2, L0731: 2, L0758: 2, L0588: 2, H0556: 1, S0282: 1, H0662: 1, H0402: 1, S0418: 1, T0008: 1, S0222: 1, H0392: 1, H0333: 1, L0021: 1, H0581: 1, S0049: 1, L0471: 1, H0266: 1, L0351: 1, L0772: 1, L0766: 1, L0776: 1, L0659: 1, L0792: 1, H0522: 1, S0027: 1, L0779: 1 and S0011: 1. | | | |
| 393 | HIBDE74 | 766011 | 403 | 99 - 362 | 1016 | | | | AR089: 1, AR061: 1 L0759: 2, H0171: 1, T0010: 1, H0090: 1, L0761: 1, L0766: 1, S3014: 1, L0745: 1, L0747: 1 and H0506: 1. | | | |
| | | 909876 | 621 | 2 - 751 | 1234 | | | | | | | |
| 394 | HWMAE53 | 909877 | 404 | 1 - 438 | 1017 | Glu-7 to Gln-17, Tyr-27 to Cys-32, Thr-63 to Lys-70, Glu-89 to Lys-94, | | | AR089: 3, AR061: 1 S0354: 1 and H0030: 1. | | | |

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| 398 | HTXJA84 | 911387 | 408 | 2 - 628 | 1021 | Arg-1 to Ser-6, Asn-55 to Phe-64, Ser-86 to Gly-92, Leu-124 to Glu-146. | | | AR061: 5, AR089: 2 H0521: 4, H0457: 3, H0580: 2, L0749: 2, L0588: 2, H0556: 1, H0485: 1, H0635: 1, H0581: 1, H0251: 1, H0124: 1, H0551: 1, H0529: 1, L0667: 1, L0773: 1, L0803: 1, S0052: 1, H0593: 1 and S0424: 1. | | | |
| 399 | HKAAW89 | 911389 | 409 | 1 - 447 | 1022 | Gln-12 to Pro-20, Thr-37 to Glu-42, Ile-49 to Arg-56. | | | AR089: 0, AR061: 0 H0494: 1, H0520: 1, H0435: 1 and H0423: 1. | | | |

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| | | | | | | Leu-75 to Arg-88, Ala-111 to Leu-118. | | | | |
| 400 | HSXDD55 | 911460 | 410 | 312 - 737 | 1023 | Arg-75 to Lys-83, Ser-89 to Arg-102, Met-136 to Arg-142. | AR061: 2, AR089: 2 L0439: 2, L0617: 1, S0356: 1, H0457: 1, S0036: 1, H0547: 1, L0758: 1 and L0608: 1. | | | |
| 401 | HUFCI64 | 911558 | 411 | 3 - 773 | 1024 | Ala-89 to Glu-98, Leu-117 to Ala-123, Glu-139 to Gly-147, Leu-158 to Thr-163, Glu-195 to Arg-211. | AR089: 14, AR061: 4 H0436: 11, H0255: 7, H0559: 7, H0521: 7, H0254: 4, H0423: 4, H0265: 3, H0486: 3, H0250: 3, H0581: 3, H0271: 3, H0124: 3, H0264: 3, H0555: 3, H0341: 2, S0354: 2, H0580: 2, H0370: 2, H0586: 2, H0257: 2, H0069: 2, H0083: 2, H0031: 2, H0634: 2, H0488: 2, S0422: 2, S0426: 2, L0766: 2, L0649: 2, L0805: 2, L0653: 2, L0776: 2, L0655: 2, L0731: 2, H0445: 2, H0543: 2, | 19p13.3 | 108725, 120700, 133171, 136836, 145981, 147141, 164953, 188070, 600957, 601238, 601846, 602216, 602477 | |

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| 402 | HWAF84 | 911559 | 412 | 1 - 702 | 1025 | | | H0677: 2, H0556: 1, H0584: 1, H0140: 1, H0583: 1, H0656: 1, H0402: 1, H0305: 1, H0458: 1, S0140: 1, H0550: 1, H0497: 1, H0575: 1, S0474: 1, H0421: 1, H0024: 1, H0213: 1, H0087: 1, H0272: 1, H0641: 1, S0144: 1, L0763: 1, L0761: 1, L0662: 1, L0794: 1, L0803: 1, L0804: 1, L0659: 1, L0787: 1, L0666: 1, L0663: 1, H0518: 1, S0044: 1, H0576: 1, L0756: 1, H0422: 1, S0452: 1 and H0506: 1. | AR061: 2, AR089: 1 | 19p13.3 | 108725, 120700, 133171, 136836, 145981, 147141, 164953, |
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| 403 | HETCL18 | 914535 | 413 | 1 - 684 | 1026 | Lys-12 to Pro-22, Lys-38 to Thr-45, Glu-65 to Lys-70, Phe-78 to Gly-83, Arg-96 to Glu-102, Leu-112 to Arg-124, Gly-139 to Ala-147, Asn-181 to Arg-186, Asn-193 to Ser-205, Leu-209 to Thr-220. | AR054: 8, AR061: 5, AR089: 5, AR050: 1, AR051: 1 L0754: 45, L0747: 8, H0553: 7, L0775: 5, L0755: 5, L0659: 4, H0046: 3, H0622: 3, H0124: 3, L0665: 3, H0660: 3, L0748: 3, L0751: 3, H0402: 2, H0438: 2, H0586: 2, H0427: 2, H0599: 2, H0575: 2, H0050: 2, L0471: 2, H0644: 2, H0616: 2, H0056: 2, L0764: 2, L0662: 2, L0794: 2, L0803: 2, L0804: 2, L0666: 2, L0663: 2, H0144: 2, L0749: 2, L0750: 2, | | 188070, 600957, 601238, 601846, 602216, 602477 |
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| | | | | | | L0777: 2, S0026: 2, H0583: 1, S0282: 1, H0305: 1, S0356: 1, S0358: 1, S0045: 1, S0046: 1, H0619: 1, H0485: 1, S0280: 1, H0042: 1, H0569: 1, H0024: 1, H0051: 1, H0071: 1, H0355: 1, H0510: 1, H0328: 1, H0615: 1, H0428: 1, H0030: 1, L0142: 1, S0364: 1, H0361: 1, H0040: 1, H0413: 1, H0059: 1, S0038: 1, L0763: 1, L0770: 1, L0769: 1, L0800: 1, L0644: 1, L0363: 1, L0806: 1, L0657: 1, L0783: 1, L0809: 1, L0664: 1, H0519: 1, H0690: 1, H0670: 1, H0672: 1, S0146: 1, H0555: 1, H0479: 1, S3012: 1, S0028: 1, L0779: 1, L0731: 1, | | | | | |
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| 404 | HCRNK75 | 914536 | 414 | 2156 - 912 | 1027 | Pro-1 to Met-7, Ala-16 to Gly-24, Gly-26 to Leu-33, Lys-57 to Pro-67, Lys-83 to Thr-90, Glu-110 to Lys-115, Phe-123 to Gly-128, Arg-141 to Glu-147, Leu-157 to Arg-169, Gly-184 to Ala-192, Asn-226 to Arg-231, Asn-238 to Ser-250, Leu-254 to Thr-265. | S0031: 1, L0605: 1, L0599: 1, L0604: 1, L0603: 1, L0366: 1, S0192: 1, H0543: 1, S0424: 1 and H0506: 1. AR061: 124, AR089: 76 L0775: 4, H0046: 3, H0622: 3, H0660: 3, H0438: 2, L0663: 2, L0665: 2, L0777: 2, S0026: 2, H0583: 1, S0282: 1, S0356: 1, H0051: 1, H0071: 1, H0355: 1, H0510: 1, H0615: 1, H0428: 1, H0644: 1, L0142: 1, S0364: 1, H0059: 1, L0763: 1, L0803: 1, L0804: 1, L0657: 1, L0809: 1, L0664: 1, H0690: 1, H0670: 1, H0672: 1, H0479: 1, S0028: 1, L0751: 1, S0031: 1, L0604: 1, L0366: 1, S0192: 1 and | | |
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| H0650: 1, H0656: 1, S0212: 1, H0306: 1, H0305: 1, S0360: 1, S0046: 1, H0619: 1, S0222: 1, S6014: 1, H0613: 1, H0492: 1, H0250: 1, H0635: 1, H0427: 1, L0021: 1, H0036: 1, H0421: 1, H0399: 1, H0416: 1, H0188: 1, S0250: 1, L0143: 1, H0617: 1, H0673: 1, H0124: 1, H0163: 1, H0634: 1, H0087: 1, T0067: 1, H0264: 1, H0272: 1, H0412: 1, H0413: 1, H0100: 1, S0344: 1, S0426: 1, L0770: 1, L0638: 1, L0761: 1, L0794: 1, L0650: 1, L0661: 1, L0546: 1, S0053: 1, H0689: 1, H0521: 1, S3014: 1, L0748: 1, L0740: 1, L0779: 1, L0780: 1, |
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| 407 | HWLFJ01 | 928017 | 417 | 1 - 780 | 1030 | Arg-11 to Arg-19, Ser-36 to Thr-61, Glu-79 to Glu-84, Ala-100 to Gln-106, Ser-155 to Leu-161. | L0753: 1, L0759: 1, H0445: 1, H0595: 1, L0362: 1, H0653: 1 and H0506: 1. | | |
| | | | | | | | AR061: 3, AR089: 2 L0741: 12, L0744: 6, H0052: 5, H0040: 5, L0742: 5, L0748: 5, H0620: 4, L0794: 4, H0486: 3, H0622: 3, L0439: 3, L0749: 3, L0777: 3, S0354: 2, H0046: 2, H0031: 2, H0617: 2, L0770: 2, L0761: 2, L0806: 2, S0126: 2, H0539: 2, H0518: 2, H0521: 2, L0751: 2, L0747: 2, L0758: 2, L0593: 2, H0624: 1, H0171: 1, S0114: 1, H0650: 1, S0418: 1, S0420: 1, H0645: 1, H0351: 1, H0370: 1, H0600: 1, H0592: 1, L0622: 1, T0082: 1, S0474: 1, | | |

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| 408 | HTXNG95 | 928577 | 418 | 13 - 594 | 1031 | Arg-41 to Thr-53, Ser-89 to Glu-95, Leu-109 to Lys-114, Pro-189 to Glu-194. | AR054: 26, AR051: 12, AR050: 10, AR061: 7, AR089: 4 H0556: 4, L0770: 4, L0794: 4, L0758: 4, L0731: 3, H0038: 2, L0766: 2, L0659: 2, S0212: 1, S0132: 1, | H0085: 1, H0235: 1, H0545: 1, H0012: 1, H0644: 1, H0124: 1, H0634: 1, H0494: 1, S0144: 1, S0142: 1, L0638: 1, L0642: 1, L0764: 1, L0771: 1, L0773: 1, L0768: 1, L0649: 1, L0774: 1, L0775: 1, L0651: 1, L0653: 1, L0776: 1, L0659: 1, L0809: 1, S0374: 1, H0690: 1, H0522: 1, H0696: 1, L0740: 1, L0754: 1, L0755: 1, L0731: 1, L0757: 1, H0707: 1, L0601: 1 and H0543: 1. | | |
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| | | | | | | | | | H0632: 1, H0618: 1, H0271: 1, S0368: 1, H0673: 1, L0667: 1, L0662: 1, L0767: 1, L0768: 1, L0381: 1, L0789: 1, L0790: 1, L0664: 1, L0665: 1, H0659: 1, H0658: 1, S0328: 1, S0454: 1, L0749: 1, L0777: 1, H0542: 1 and H0677: 1. | | | |
| 409 | HPCIG66 | 930886 | 419 | 30 - 653 | 1032 | Asn-48 to Gly-54, Thr-56 to Lys-69. | | | AR089: 1, AR061: 0 H0642: 2 and S0053: 1. | | | |
| 410 | HCRPU72 | 931140 | 420 | 2 - 799 | 1033 | Gly-1 to Val-11, Gly-50 to Thr-62, Asn-125 to Gly-132, Leu-172 to Asn-178, Ser-210 to Ser-217, Ser-232 to Lys-245. | | | AR089: 16, AR061: 6 H0144: 6, H0013: 2 and S0356: 1. | | | |
| 411 | HE9RT95 | 934556 | 421 | 1 - 714 | 1034 | Leu-21 to Asp-33. | | | AR089: 17, AR061: 13 S0049: 1, H0144: 1 and L0439: 1. | | | |
| 412 | HFXJM13 | 935725 | 422 | 16 - 438 | 1035 | Gln-36 to Thr-42, Glu-99 to Leu-104. | | | AR061: 1, AR089: 0 L0748: 7, L0766: 6, L0756: 5, H0580: 4, L0777: 3, H0052: 2, | | | |

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|--|--|--|--|--|--|--|--|
| | S0051: 2, H0644: 2, H0551: 2, L0769: 2, H0144: 2, L0743: 2, L0754: 2, L0779: 2, L0755: 2, L0759: 2, H0657: 1, H0656: 1, S0116: 1, H0341: 1, S0212: 1, S0282: 1, H0125: 1, L0005: 1, S0222: 1, H0431: 1, H0438: 1, H0586: 1, H0069: 1, H0635: 1, L0157: 1, H0050: 1, L0471: 1, H0051: 1, H0399: 1, H0375: 1, S0318: 1, S0316: 1, H0687: 1, S0250: 1, H0031: 1, H0553: 1, H0090: 1, H0634: 1, H0616: 1, H0623: 1, S0038: 1, H0100: 1, L0371: 1, L0667: 1, L0800: 1, L0794: 1, L0804: 1, L0775: 1, L0805: 1, L0776: 1, L0659: 1, L0526: 1, | | | | | | |
|--|--|--|--|--|--|--|--|

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|-----|---------|--------|-----|----------|------|--|---|---------|--|--|--|--|
| | | | | | | | | | L0792: 1, L0663: 1, L0438: 1, H0547: 1, S0126: 1, L0439: 1, L0740: 1, L0749: 1, L0752: 1, S0031: 1, H0445: 1, L0480: 1, L0604: 1, S0026: 1, H0542: 1, S0412: 1 and H0352: 1. | | | |
| 413 | HDPWU37 | 940705 | 423 | 3 - 536 | 1036 | Glu-8 to Pro-17, Pro-31 to Asp-37. | AR089: 12, AR061: 6 H0575: 1, H0271: 1 and H0521: 1. | 22q13.1 | 103050, 103050, 124030, 124030, 138981, 182380, 188826, 190040, 190040, 190040 | | | |
| 414 | HHSDL85 | 942246 | 424 | 2 - 502 | 1037 | Ser-12 to Gln-25, Pro-29 to Phe-39, Gly-81 to Gly-89, Glu-143 to Trp-156. | AR061: 3, AR089: 2 S0007: 3, S0001: 1, H0618: 1, H0009: 1, S0051: 1, L0763: 1, L0439: 1 and L0758: 1. | | | | | |
| | | 951168 | 622 | 356 - 42 | 1235 | Arg-82 to Trp-88. | | | | | | |
| 415 | HTJMD31 | 942848 | 425 | 1 - 462 | 1038 | Pro-17 to Asn-23. | AR089: 14, AR061: 6 | | | | | |

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|-----|---------|--------|-----|------------|------|---|---|--|--|--|--|
| | | | | | | | | S0300: 2, L0439: 2, H0438: 1, H0618: 1, H0052: 1, H0616: 1, H0488: 1, L0772: 1, L0806: 1, L0384: 1, L0666: 1, L0758: 1 and H0423: 1. | | | |
| 416 | HWADD57 | 943039 | 426 | 2 - 1009 | 1039 | Asp-2 to Pro-7, Leu-18 to Arg-27, Glu-52 to Ser-59, Pro-90 to Pro-97, Pro-116 to Glu-121. | AR089: 1, AR061: 0 H0255: 2, H0486: 1, H0581: 1, H0529: 1 and H0543: 1. | | | | |
| 417 | HLWAH05 | 944904 | 427 | 356 - 1351 | 1040 | Ala-1 to Arg-9, Leu-11 to Pro-18. | AR061: 2, AR089: 1 H0586: 5, L0751: 2, H0170: 1, H0638: 1, H0553: 1, H0477: 1, S0002: 1, H0529: 1, L0766: 1, L0803: 1, H0672: 1 and H0543: 1. | | | | |
| 418 | HDPCI84 | 945527 | 428 | 25 - 1047 | 1041 | Arg-9 to Arg-18, Leu-107 to Gln-113, Asp-126 to Thr-131. | AR089: 2, AR061: 1 H0521: 4, L0803: 3, S0358: 2, H0489: 2, H0046: 2, L0794: 2, L0666: 2, H0144: 2, S0126: 2, S0342: 1, H0663: 1, S0356: 1, | | | | |

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|-----|---------|--------|-----|-----------|------|--|--|--|--|
| 419 | HBXDJ07 | 946830 | 429 | 125 - 652 | 1042 | Glu-62 to Lys-68, Asn-105 to Gly-113. | H0013: 1, L0021: 1, H0705: 1, H0150: 1, H0266: 1, H0039: 1, H0622: 1, H0038: 1, H0551: 1, S0422: 1, L0598: 1, L0646: 1, L0766: 1, L0653: 1, L0656: 1, L0789: 1, L0532: 1, L0663: 1, H0658: 1, L0748: 1, L0759: 1, S0434: 1, L0596: 1 and H0506: 1, AR061: 2, AR089: 2, L0439: 11, L0794: 5, L0666: 5, S0222: 4, H0052: 3, L0756: 3, H0624: 2, S6028: 2, S0038: 2, L0638: 2, L0805: 2, L0664: 2, L0438: 2, L0740: 2, H0171: 1, S6024: 1, H0013: 1, H0374: 1, H0050: 1, S0050: 1, H0051: 1, S0386: 1, L0769: 1, L0768: 1, L0776: 1, L0659: 1, | | |
|-----|---------|--------|-----|-----------|------|--|--|--|--|

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|-----|---------|--------|-----|---------|------|--|---|--|--|
| 420 | HAMFD12 | 952438 | 430 | 3 - 539 | 1043 | Tyr-41 to Leu-52, Leu-64 to Cys-72, Pro-92 to Arg-98, Ser-110 to Glu-116. | L0789: 1, H0144: 1, L0745: 1 and L0746: 1. AR089: 3, AR061: 1 H0271: 10, H0052: 8, H0556: 7, L0439: 7, L0754: 7, H0622: 6, L0776: 5, L0769: 4, H0265: 3, H0295: 3, H0580: 3, S0222: 3, H0013: 3, H0156: 3, H0051: 3, H0494: 3, L0659: 3, S0356: 2, H0208: 2, S6014: 2, H0135: 2, H0634: 2, S0002: 2, S0426: 2, L0770: 2, L0796: 2, L0373: 2, L0803: 2, L0375: 2, L0655: 2, L0666: 2, L0438: 2, H0672: 2, H0521: 2, L0747: 2, L0750: 2, L0756: 2, L0588: 2, H0542: 2, H0543: 2, H0170: 1, S0212: 1, S0282: 1, S0030: 1, H0305: 1, H0589: 1, | | |
|-----|---------|--------|-----|---------|------|--|---|--|--|

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|--|--|--|--|--|--|--|
| | | | | | | L0619: 1, H0619: 1, S6026: 1, H0550: 1, H0370: 1, H0600: 1, H0592: 1, H0486: 1, T0040: 1, H0635: 1, H0002: 1, S0010: 1, H0390: 1, H0581: 1, H0421: 1, H0085: 1, T0110: 1, H0041: 1, N0006: 1, H0050: 1, H0012: 1, H0620: 1, T0003: 1, H0024: 1, H0687: 1, H0252: 1, H0604: 1, H0031: 1, H0644: 1, H0628: 1, H0598: 1, H0087: 1, H0264: 1, S0112: 1, T0041: 1, H0560: 1, S0150: 1, H0529: 1, L0640: 1, L0761: 1, L0643: 1, L0806: 1, L0658: 1, L0809: 1, L0544: 1, L0788: 1, L0663: 1, L0664: 1, L0665: 1, S0428: 1, S0053: 1, H0144: 1, |
|--|--|--|--|--|--|--|

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|-----|---------|--------|-----|------------|------|--|--|--|--|--|
| | | | | | | | H0690: 1, H0518: 1, H0696: 1, H0436: 1, H0576: 1, S0392: 1, L0740: 1, L0731: 1, L0759: 1, S0031: 1, L0596: 1, S0011: 1, H0667: 1 and S0192: 1. | | | |
| 421 | HFKHR40 | 952470 | 431 | 641 - 1756 | 1044 | Gly-18 to His-25. | AR089: 1, AR061: 0 H0457: 7, H0521: 2, H0656: 1, H0458: 1, S0278: 1, H0069: 1, H0620: 1, H0179: 1, H0271: 1, H0416: 1, S0144: 1, H0703: 1, H0593: 1 and H0522: 1. | | | |
| 422 | HDTAI08 | 953265 | 432 | 316 - 567 | 1045 | Leu-13 to Val-25, His-32 to Arg-39. | AR061: 1, AR089: 1 H0521: 4, H0580: 2, H0583: 1, H0486: 1, H0625: 1, S0466: 1, L0666: 1, S0242: 1, H0542: 1 and H0543: 1. | | | |
| 423 | HMKCX80 | 956254 | 433 | 194 - 616 | 1046 | Gln-7 to Asp-19, Leu-34 to Ser-42. | AR089: 7, AR061: 3 H0392: 1, H0427: 1, H0318: 1, L0663: 1, H0345: 1 and L0596: 1. | | | |
| 424 | HCEMF69 | 961308 | 434 | 2 - 637 | 1047 | | AR061: 1, AR089: 1 | | | |

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|-----|---------|--------|-----|------------|------|-------------------|---|--|--|--|
| 425 | HWLHF10 | 963422 | 435 | 115 - 978 | 1048 | Ile-44 to Gln-50. | AR089: 26, AR061: 4 S0354: 1, H0561: 1 and L0603: 1. | | | S0136: 3, L0779: 3, H0171: 1, H0052: 1, H0038: 1, L0766: 1, H0547: 1, S0031: 1 and S0242: 1. |
| 426 | HOEMG82 | 963855 | 436 | 2 - 991 | 1049 | Asp-1 to Pro-12. | AR061: 49, AR089: 19 | | | |
| 427 | HFXDR37 | 965915 | 437 | 1485 - 556 | 1050 | Glu-18 to Thr-23. | AR061: 2, AR089: 1 L0766: 2, S0001: 1, H0592: 1, H0575: 1, H0644: 1, H0038: 1 and H0144: 1. | | | |
| 428 | HNNAS46 | 969470 | 438 | 1 - 834 | 1051 | | AR089: 1, AR061: 0 H0638: 2, H0521: 2, L0752: 2, H0677: 2, H0650: 1, H0484: 1, H0458: 1, H0580: 1, H0586: 1, H0575: 1, H0081: 1, S0036: 1, H0063: 1, H0560: 1, L0809: 1, S0126: 1, S0328: 1, L0744: 1, L0740: 1, L0754: 1 and | | | |

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|-----|---------|--------|-----|----------|------|--|---|--|--|
| 429 | HRAAS26 | 971219 | 439 | 17 - 535 | 1052 | Glu-25 to Arg-31, Glu-71 to His-76, Leu-85 to Leu-92, Gly-129 to Ser-143. | H0543: 1. AR054: 23, AR050: 18, AR051: 12, AR061: 12, AR089: 8 L0803: 7, L0794: 4, L0748: 4, L0591: 4, L0770: 3, L0804: 3, S0142: 2, L0789: 2, L0743: 2, L0747: 2, L0749: 2, L0752: 2, S0360: 1, S0046: 1, H0549: 1, H0309: 1, H0327: 1, H0012: 1, L0769: 1, L0773: 1, L0767: 1, L0774: 1, L0775: 1, L0776: 1, L0790: 1, L0791: 1, H0435: 1, H0660: 1, H0648: 1, H0521: 1, H0555: 1, L0750: 1, L0779: 1, L0777: 1, L0755: 1, L0758: 1 and S0434: 1. | | |
| 430 | HHEEL28 | 973096 | 440 | 1 - 378 | 1053 | | AR089: 1, AR061: 0 L0766: 7, H0486: 4, L0794: 4, H0520: 4, | | |

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|-----|---------|--------|-----|------------|------|--------------------------------------|--|--|--|
| 431 | HCETF22 | 973324 | 441 | 112 - 1863 | 1054 | Asn-1 to Gly-9, Gln-30 to Glu-35. | S0374: 1, H0435: 1, H0670: 1, H0651: 1, H0521: 1, H0436: 1, H0345: 1, L0439: 1, L0745: 1, L0749: 1, L0750: 1, L0759: 1, L0485: 1, L0593: 1, S0026: 1, H0665: 1, H0543: 1, H0423: 1, H0422: 1 and S0458: 1. | | |
| | | | | | | | AR061: 11, AR089: 4 L0741: 8, L0766: 7, L0794: 6, H0306: 4, H0052: 4, L0768: 3, L0803: 3, H0542: 3, S0360: 2, H0457: 2, H0617: 2, H0606: 2, S0036: 2, H0100: 2, L0800: 2, H0672: 2, H0436: 2, L0777: 2, H0543: 2, H0650: 1, L0785: 1, H0341: 1, H0254: 1, H0402: 1, S0420: 1, H0580: 1, S0045: 1, H0645: 1, H0550: 1, S0222: 1, | | |

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|-----|---------|--------|-----|-----------|------|--|--|--|--|--|--|--|--|
| | | | | | | | | S6014: 1, H0592: 1, N0009: 1, S0280: 1, H0599: 1, H0618: 1, S0182: 1, H0581: 1, S0049: 1, H0194: 1, N0007: 1, H0271: 1, H0252: 1, H0063: 1, H0488: 1, H0412: 1, H0079: 1, T0041: 1, H0646: 1, S0144: 1, L0763: 1, L0770: 1, L0769: 1, L0761: 1, L0372: 1, L0646: 1, L0645: 1, L0764: 1, L0774: 1, L0792: 1, L0666: 1, L0665: 1, H0519: 1, H0435: 1, H0539: 1, H0518: 1, L0747: 1, L0755: 1, H0653: 1, H0136: 1, H0677: 1 and S0446: 1. | | | | | |
| 432 | HCMSF55 | 912284 | 442 | 657 - 361 | 1055 | | | AR089: 2, AR061: 2 L0604: 16, S0366: 9, L0485: 7, L0622: 6, L0623: 6, H0599: 6, H0373: 6, H0196: 4, | | | | | |

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| | | | | | | L0163: 4, L0777: 4, L0520: 3, H0002: 2, S0364: 2, S0330: 2, L0747: 2, H0171: 1, H0549: 1, H0486: 1, H0013: 1, H0253: 1, H0318: 1, S0049: 1, H0251: 1, L0471: 1, S0051: 1, H0616: 1, S0038: 1, H0100: 1, H0561: 1, L0803: 1, L0782: 1, L0809: 1, L0779: 1, L0759: 1 and L0584: 1. | |
| | 975280 | 623 | 52 - 705 | 1236 | His-10 to Gly-16, Pro-65 to Ala-70, Ala-96 to Lys-101. | | |

[51] The first column in Table 1A provides the gene number in the application corresponding to the clone identifier. The second column in Table 1A provides a unique "Clone ID NO:Z" for a cDNA clone related to each contig sequence disclosed in Table 1A. This clone ID references the cDNA clone which contains at least the 5' most sequence of the assembled contig and at least a portion of SEQ ID NO:X was determined by directly sequencing the referenced clone. The reference clone may have more sequence than described in the sequence listing or the clone may have less. In the vast majority of cases, however, the clone is believed to encode a full-length polypeptide. In the case where a clone is not full-length, a full-length cDNA can be obtained by methods described elsewhere herein.

[52] The third column in Table 1A provides a unique "Contig ID" identification for each contig sequence. The fourth column provides the "SEQ ID NO:" identifier for each of the contig polynucleotide sequences disclosed in Table 1A. The fifth column, "ORF (From-To)", provides the location (i.e., nucleotide position numbers) within the polynucleotide sequence "SEQ ID NO:X" that delineate the preferred open reading frame (ORF) shown in the sequence listing and referenced in Table 1A, column 6, as SEQ ID NO:Y. Where the nucleotide position number "To" is lower than the nucleotide position number "From", the preferred ORF is the reverse complement of the referenced polynucleotide sequence.

[53] The sixth column in Table 1A provides the corresponding SEQ ID NO:Y for the polypeptide sequence encoded by the preferred ORF delineated in column 5. In one embodiment, the invention provides an amino acid sequence comprising, or alternatively consisting of, a polypeptide encoded by the portion of SEQ ID NO:X delineated by "ORF (From-To)". Also provided are polynucleotides encoding such amino acid sequences and the complementary strand thereto.

[54] Column 7 in Table 1A lists residues comprising epitopes contained in the polypeptides encoded by the preferred ORF (SEQ ID NO:Y), as predicted using the algorithm of Jameson and Wolf, (1988) Comp. Appl. Biosci. 4:181-186. The Jameson-Wolf antigenic analysis was performed using the computer program PROTEAN (Version 3.11 for the Power MacIntosh, DNASTAR, Inc., 1228 South Park Street Madison, WI). In specific embodiments, polypeptides of the invention comprise, or alternatively consist of, at least one, two, three, four, five or more of the predicted epitopes as described in Table 1A. It will be appreciated that depending on the analytical criteria used to predict antigenic determinants, the exact address of the determinant may vary slightly.

[55] Column 8 in Table 1A provides an expression profile and library code: count for each of the contig sequences (SEQ ID NO:X) disclosed in Table 1A, which can routinely be combined with the information provided in Table 4 and used to determine the tissues, cells, and/or cell line libraries which predominantly express the polynucleotides of the invention. The first number in column 8 (preceding the colon), represents the tissue/cell source identifier code corresponding to the code and description provided in Table 4. For those identifier codes in which the first two letters are not "AR", the second number in column 8 (following the colon) represents the number of times a sequence corresponding to the reference polynucleotide sequence was identified in the tissue/cell source. Those tissue/cell source identifier codes in which the first two letters are "AR" designate information generated using DNA array technology. Utilizing this technology, cDNAs were amplified by PCR and then transferred, in duplicate, onto the array. Gene expression was assayed through hybridization of first strand cDNA probes to the DNA array. cDNA probes were generated from total RNA extracted from a variety of different tissues and cell lines. Probe synthesis was performed in the presence of ³³P dCTP, using oligo(dT) to prime reverse transcription. After hybridization, high stringency washing conditions were employed to remove non-specific hybrids from the array. The remaining signal, emanating from each gene target, was measured using a Phosphorimager. Gene expression was reported as Phosphor Stimulating Luminescence (PSL) which reflects the level of phosphor signal generated from the probe hybridized to each of the gene targets represented on the array. A local background signal subtraction was performed before the total signal generated from each array was used to normalize gene expression between the different hybridizations. The value presented after "[array code]:" represents the mean of the duplicate values, following background subtraction and probe normalization. One of skill in the art could routinely use this information to identify normal and/or diseased tissue(s) which show a predominant expression pattern of the corresponding polynucleotide of the invention or to identify polynucleotides which show predominant and/or specific tissue and/or cell expression.

[56] Column 9 in Table 1A provides a chromosomal map location for certain polynucleotides of the invention. Chromosomal location was determined by finding exact matches to EST and cDNA sequences contained in the NCBI (National Center for Biotechnology Information) UniGene database. Each sequence in the UniGene database is assigned to a "cluster"; all of the ESTs, cDNAs, and STSs in a cluster are believed to be derived from a single gene. Chromosomal mapping data is often available for one or more

sequence(s) in a UniGene cluster; this data (if consistent) is then applied to the cluster as a whole. Thus, it is possible to infer the chromosomal location of a new polynucleotide sequence by determining its identity with a mapped UniGene cluster.

[57] A modified version of the computer program BLASTN (Altshul et al., J. Mol. Biol. 215:403-410 (1990); and Gish and States, Nat. Genet. 3:266-272 (1993)) was used to search the UniGene database for EST or cDNA sequences that contain exact or near-exact matches to a polynucleotide sequence of the invention (the 'Query'). A sequence from the UniGene database (the 'Subject') was said to be an exact match if it contained a segment of 50 nucleotides in length such that 48 of those nucleotides were in the same order as found in the Query sequence. If all of the matches that met this criteria were in the same UniGene cluster, and mapping data was available for this cluster, it is indicated in Table 1A under the heading "Cytologic Band". Where a cluster had been further localized to a distinct cytologic band, that band is disclosed; where no banding information was available, but the gene had been localized to a single chromosome, the chromosome is disclosed.

[58] Once a presumptive chromosomal location was determined for a polynucleotide of the invention, an associated disease locus was identified by comparison with a database of diseases which have been experimentally associated with genetic loci. The database used was the Morbid Map, derived from OMIM™ (*supra*). If the putative chromosomal location of a polynucleotide of the invention (Query sequence) was associated with a disease in the Morbid Map database, an OMIM reference identification number was noted in column 10, Table 1A, labelled "OMIM Disease Reference(s)". Table 5 is a key to the OMIM reference identification numbers (column 1), and provides a description of the associated disease in Column 2.

TABLE 1B

| Clone ID NO:Z | SEQ ID NO:X | CONTIG ID: | BAC ID: A | SEQ ID NO:B | EXON From-To |
|------------------|----------------|---------------|-----------|----------------|--|
| HFCBB56 | 24 | 910073 | AC068296 | 1268 | 1-225 |
| HIBBF63 | 75 | 912715 | AC009065 | 1269 | 1-70 850-1112 1169-1622 1707-1779 1874-1924 2836-2908 3006-4160 |
| HIBBF63 | 75 | 912715 | AC012171 | 1270 | 1-64 159-209 1122-1194 1292-1527 1593-2446 |
| HIBBF63 | 75 | 912715 | AC005346 | 1271 | 1-70 874-1136 1193-1646 1731-1803 1898-1948 2861-2933 3031-4185 |
| HIBBF63 | 75 | 912715 | AC009065 | 1272 | 1-547 |
| HIBBF63 | 75 | 912715 | AC012171 | 1273 | 1-547 |
| HIBBF63 | 75 | 912715 | AC009065 | 1274 | 1-424 |
| HIBBF63 | 75 | 912715 | AC005346 | 1275 | 1-547 |
| HIBBF63 | 75 | 912715 | AC012171 | 1276 | 1-419 |
| HIBBF63 | 75 | 912715 | AC005346 | 1277 | 1-424 |
| H2CBH45 | 90 | 963811 | AC068243 | 1278 | 1-267 1540-1640 3095-3380 3393-3556 3901-3967 4137-4639 5287-5856 5916-6588 7029-7876 8324-8414 |
| H2CBH45 | 90 | 963811 | AC068243 | 1279 | 1-309 |
| HBGQT03 | 93 | 908173 | AC024045 | 1280 | 1-218 |

| | | | | | |
|---------|-----|--------|----------|------|---|
| | | | | | 457-549 660-819 2039-2238 2529-2763 2876-3033 3631-3810 3941-4058 4184-4322 4727-4851 5161-6181 |
| HBGQT03 | 93 | 908173 | AC024045 | 1281 | 1-176 |
| HBGQT03 | 93 | 908173 | AC024045 | 1282 | 1-461 960-1030 1194-1959 2041-2516 3037-3122 3396-3455 4055-4366 4547-4599 4967-5216 5321-5461 6521-7174 7564-7841 8311-8758 8829-8969 8997-10118 10257-10910 12058-12385 12438-12953 13729-13873 |
| HCEPH71 | 97 | 522739 | AL365319 | 1283 | 1-494 |
| HCEPH71 | 97 | 522739 | AL390715 | 1284 | 1-494 |
| HCOOZ11 | 100 | 965306 | AL022238 | 1285 | 1-121 899-983 1445-1513 2166-3430 3550-3763 3859-3972 4449-4595 4960-5152 5385-5529 |

| | | | | | |
|---------|-----|--------|----------|------|--|
| | | | | | 5744-5972 6327-7067 7097-7152 7210-8073 8079-8680 8772-11399 12956-13517 13736-14155 14311-14753 16294-16357 16648-16806 16874-17059 17685-17787 |
| HCOOZ11 | 100 | 965306 | AL022238 | 1286 | 1-540 |
| HCOOZ11 | 100 | 965306 | AL022238 | 1287 | 1-665 |
| HCWFF88 | 101 | 506577 | AC025670 | 1288 | 1-300 |
| HCWFF88 | 101 | 506577 | AL157951 | 1289 | 1-624 |
| HCWFF88 | 101 | 506577 | AL157951 | 1290 | 1-409 |
| HCWFF88 | 101 | 506577 | AL157951 | 1291 | 1-83 |
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| HAPNZ77 | 359 | 887072 | AC076973 | 1449 | 1-480 |
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| HTSFJ40 | 364 | 722406 | AL161645 | 1455 | 1-247 1217-1320 1624-1963 2076-2179 2604-2711 2716-3114 3399-3638 4344-4427 5079-5141 5439-8153 8268-8798 |
| HTSFJ40 | 364 | 722406 | AC006171 | 1456 | 1-2213 |
| HSDJH12 | 368 | 876344 | AC021747 | 1457 | 1-76 239-328 886-973 3912-4047 6397-6453 7393-7574 8590-9069 9354-10839 13386-13803 14791-15108 15296-15408 15499-15925 16031-16317 16452-16602 17145-18449 |
| HSDJH12 | 368 | 876344 | AL359882 | 1458 | 1-283 1271-1588 1793-1888 1979-2405 |
| HSDJH12 | 368 | 876344 | AC046143 | 1459 | 1-283 1272-1589 1794-1889 1980-2406 2512-2797 2932-3082 |
| HWLEY40 | 374 | 957875 | AC006171 | 1460 | 1-247 1217-1320 1624-1963 |

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|---------|-----|--------|----------|------|---|
| | | | | | 2076-2179 2604-2711 2716-3114 3399-3638 4344-4427 5079-5141 5439-8153 8268-8798 |
| HWLEY40 | 374 | 957875 | AL161645 | 1461 | 1-247 1217-1320 1624-1963 2076-2179 2604-2711 2716-3114 3399-3638 4344-4427 5079-5141 5439-8153 8268-8798 |
| HWLEY40 | 374 | 957875 | AC006171 | 1462 | 1-2213 |
| HOUBZ94 | 376 | 527876 | AC068475 | 1463 | 1-70 163-330 651-994 1105-1272 1372-1586 2253-2908 2995-3524 3711-4406 4418-4480 4581-5218 5621-5829 6007-6286 |
| HOUBZ94 | 376 | 527876 | AC005954 | 1464 | 1-91 893-1009 1323-1695 1856-2422 3548-3650 3665-4010 4965-5170 5288-5397 6874-7000 |

| | | | | | |
|---------|-----|--------|----------|------|---|
| | | | | | 7283-7430 7520-7600 7693-7860 8181-8524 8634-8807 8902-9116 9783-10438 10525-11054 11241-11936 11948-12010 12111-12748 13154-13362 13540-13833 14748-14851 14928-15142 15543-15616 17091-17240 17351-18020 18331-18662 19524-19871 19999-20209 20570-20670 20861-21075 22489-22727 22961-23073 25307-25360 29573-29961 31051-31168 |
| HOUBZ94 | 376 | 527876 | AC005954 | 1465 | 1-131 |
| HCE3W04 | 379 | 615501 | AC022366 | 1466 | 1-565 1503-1718 1838-1933 2011-2097 2265-2335 2588-2693 2905-2975 3090-3726 3809-3889 4080-4591 4847-5070 5355-5819 |

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|---------|-----|--------|----------|------|--|
| HCE3W04 | 379 | 615501 | AC022506 | 1467 | 1-563 1501-1716 1836-1931 2009-2094 2263-2333 2586-2691 2903-2973 3088-3724 3807-3887 4085-4540 |
| HCE3W04 | 379 | 615501 | AC025165 | 1468 | 1-565 1503-1718 1838-1933 2011-2097 2265-2335 2588-2693 2905-2975 3090-3726 3809-3889 4080-4591 4847-5070 5355-5819 |
| HCE3W04 | 379 | 615501 | AC025165 | 1469 | 1-604 |
| HCE3W04 | 379 | 615501 | AC022506 | 1470 | 1-518 999-1533 1563-1830 2015-2094 2441-3538 4095-4315 4655-5378 |
| HPJAP28 | 382 | 686349 | AC004794 | 1471 | 1-599 769-987 1562-1690 1879-2043 2595-2821 3807-5923 6102-6572 6644-7502 8127-8585 9415-9553 9669-9763 |

| | | | | | |
|---------|-----|--------|----------|------|---|
| | | | | | 9826-9989 10230-10322 |
| HPJAP28 | 382 | 686349 | AC004794 | 1472 | 1-97 1121-1975 |
| HPJAP28 | 382 | 686349 | AC004794 | 1473 | 1-691 |
| HIBEC79 | 383 | 703000 | AC011458 | 1474 | 1-138 397-1114 1356-1693 1781-2091 2270-2389 2474-2908 3053-3202 3288-3349 3421-3976 4551-4662 4696-5053 5166-5246 5318-5490 5592-5723 6082-6283 6619-6733 6853-6942 7491-7586 7922-8003 8015-8421 8432-8624 8714-8856 8943-10332 |
| | | | | | 10482-10901 11647-11934 13110-13177 13310-14175 |
| HIBEC79 | 383 | 703000 | AC011458 | 1475 | 1-406 |
| HIBEC79 | 383 | 703000 | AC011458 | 1476 | 1-287 |
| HNFS82 | 387 | 779946 | AC010835 | 1477 | 1-418 |
| HFPBB28 | 389 | 844526 | AC016135 | 1478 | 1-845 |
| HFPBB28 | 389 | 844526 | AC018512 | 1479 | 1-776 |
| HFPBB28 | 389 | 844526 | AC073717 | 1480 | 1-240 |
| HFPBB28 | 389 | 844526 | AC002518 | 1481 | 1-150 |
| HDQGZ78 | 399 | 909735 | AC026282 | 1482 | 1-238 976-1440 |

| | | | | | |
|---------|-----|--------|----------|------|--|
| | | | | | 2143-2356 6769-6910 9591-9648 9951-10098 |
| HSIDQ38 | 401 | 909854 | AC003070 | 1483 | 1-152 3039-3473 4301-4483 4678-4795 5280-5944 6055-6117 6290-6359 6677-6761 8475-9284 11404-11918 12112-12437 12443-13065 13153-13467 13593-13719 13799-14185 14224-16489 |
| HFTBL33 | 407 | 910055 | AC022366 | 1484 | 1-565 1503-1718 1838-1933 2011-2097 2265-2335 2588-2693 2905-2975 3090-3726 3809-3889 4080-4591 4847-5070 5355-5819 |
| HFTBL33 | 407 | 910055 | AC025165 | 1485 | 1-565 1503-1718 1838-1933 2011-2097 2265-2335 2588-2693 2905-2975 3090-3726 3809-3889 |

| | | | | | |
|---------|-----|--------|----------|------|--|
| | | | | | 4080-4591 4847-5070 5355-5819 |
| HFTBL33 | 407 | 910055 | AC025165 | 1486 | 1-604 |
| HUFCI64 | 411 | 911558 | AC004151 | 1487 | 1-145 359-443 527-599 798-868 958-1095 1196-1260 1465-1577 1652-1732 2256-3158 4031-4899 4984-5306 5735-6066 6554-6694 6780-6970 7107-7232 7316-7404 7529-7643 7744-7917 8401-8592 8675-8813 9685-9920 9958-10211 10485-11014 11088-11199 11958-15576 16324-16465 16587-16818 16939-17000 17440-17554 17558-17946 18645-18765 19015-19378 20522-20937 22111-22452 |
| HUFCI64 | 411 | 911558 | AC004151 | 1488 | 1-134 |
| HWAFT84 | 412 | 911559 | AC004151 | 1489 | 1-145 359-443 |

| | | | | | |
|---------|-----|--------|----------|------|--|
| | | | | | 527-599 798-868 958-1095 1196-1260 1465-1577 1652-1732 2256-3158 4031-4899 4984-5306 5735-6066 6554-6694 6780-6970 7107-7232 7316-7404 7529-7643 7744-7917 8401-8592 8675-8813 9685-9920 9958-10211 10485-11014 11088-11199 11958-15576 16324-16465 16587-16818 16939-17000 17440-17554 17558-17946 18645-18765 19015-19378 20522-20937 22111-22452 |
| HWAFT84 | 412 | 911559 | AC004151 | 1490 | 1-134 |
| HWADR60 | 416 | 926487 | AC023176 | 1491 | 1-178 293-506 542-940 1591-2005 2031-2104 2390-2509 3681-3797 4018-4165 |

| | | | | | |
|---------|-----|--------|----------|------|---|
| | | | | | 4267-4381 4704-4736 |
| HWADR60 | 416 | 926487 | AC023176 | 1492 | 1-162 443-739 1067-1458 1745-1877 1976-2119 2816-2883 3171-3294 3727-4154 4340-4442 5251-6126 6708-7176 7418-7880 8134-8752 9979-10164 11234-11413 12532-12666 13313-13459 14761-14898 15208-15308 16207-16518 |
| HPCIG66 | 419 | 930886 | AC024888 | 1493 | 1-36 149-234 537-623 852-921 1077-1728 |
| HPCIG66 | 419 | 930886 | AC024888 | 1494 | 1-61 133-210 992-1107 1310-1644 1834-1905 2133-2254 2927-3032 4154-4254 4482-4683 |
| HPCIG66 | 419 | 930886 | AC024888 | 1495 | 1-63 239-327 574-1064 1763-2190 2394-2604 |

| | | | | | |
|---------|-----|--------|----------|------|---|
| | | | | | 2659-2795 3452-4040 5967-6046 6187-6254 |
| HCRPU72 | 420 | 931140 | AC023151 | 1496 | 1-65 721-1042 |
| HE9RT95 | 421 | 934556 | AC008439 | 1497 | 1-57 311-418 1581-1904 2176-2322 2625-2690 3445-3950 5254-5425 5466-5980 6002-6037 6169-6228 6339-6480 6701-6739 7238-7349 7664-8821 |
| HE9RT95 | 421 | 934556 | AC022420 | 1498 | 1-323 1372-1431 1657-1821 2377-2485 4488-4700 4954-5061 6224-6547 6819-6965 7268-7333 8088-8593 9897-10068 10109-10623 10645-10680 10812-10871 10982-11123 11345-11383 11877-12000 12310-13467 |
| HE9RT95 | 421 | 934556 | AC022420 | 1499 | 1-389 |
| HE9RT95 | 421 | 934556 | AC022420 | 1500 | 1-62 295-403 |

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|---------|-----|--------|----------|------|--|
| | | | | | 455-979 1019-1061 1466-1537 1890-2030 2114-2253 2405-2467 3328-4030 4195-4291 4697-5333 5488-5653 5816-6265 6276-6404 6478-6562 6731-6850 6982-7208 7575-7678 7732-8148 8195-8864 8885-9392 9590-9721 9859-10754 10980-11014 11126-12121 |
| HWADD57 | 426 | 943039 | AC011492 | 1501 | 1-303 949-1648 1913-2937 3032-3231 3325-3443 4093-4485 4777-4936 5057-5548 5650-5968 |
| HWADD57 | 426 | 943039 | AC011492 | 1502 | 1-50 852-907 988-1407 1584-1839 2455-2586 2689-2787 |
| HFKHR40 | 431 | 952470 | AC018805 | 1503 | 1-525 612-1372 1476-1730 |

| | | | | | |
|---------|-----|--------|----------|------|--|
| | | | | | 1732-2155 2345-2460 2652-3025 3157-3251 3449-3540 3680-3780 3914-4131 4215-4491 4603-4741 4913-4987 5135-5190 5435-5571 5901-6011 6309-6423 6922-8294 8370-8522 |
| HFKHR40 | 431 | 952470 | AC061707 | 1504 | 1-527 614-1374 1478-1732 1734-2158 2348-2463 2655-3027 3159-3253 3451-3542 3682-3782 3916-4134 4219-4495 4607-4745 4917-4991 5139-5194 5439-5575 5905-6015 6313-6427 6926-9300 9919-9960 10029-10186 11393-11624 12094-12294 13227-13375 13690-13829 13921-14010 |

| | | | | | |
|---------|-----|--------|----------|------|--|
| | | | | | 14362-14486 |
| HFKHR40 | 431 | 952470 | AC018805 | 1505 | 1-343 700-770 |
| HFKHR40 | 431 | 952470 | AC061707 | 1506 | 1-343 700-771 |
| HFKHR40 | 431 | 952470 | AC061707 | 1507 | 1-277 |
| HWLHF10 | 435 | 963422 | AC010545 | 1508 | 1-40 1661-1891 2119-2199 5160-5349 6239-6607 7675-8566 9450-9516 9675-9752 10110-10274 14154-15055 16384-16500 17055-17139 19941-20453 20703-21216 21806-21945 23638-24171 24527-24795 25564-25656 26644-26787 27284-27438 28354-28612 29247-29591 29597-30208 32018-32539 33187-33942 |
| HWLHF10 | 435 | 963422 | AC010545 | 1509 | 1-721 |
| HWLHF10 | 435 | 963422 | AC010545 | 1510 | 1-610 675-1454 1591-2267 2801-3363 |

[59] Table 1B summarizes additional polynucleotides encompassed by the invention (including cDNA clones related to the sequences (Clone ID NO:Z), contig sequences (contig identifier (Contig ID:) contig nucleotide sequence identifiers (SEQ ID NO:X)), and genomic sequences (SEQ ID NO:B). The first column provides a unique clone identifier, "Clone ID NO:Z", for a cDNA clone related to each contig sequence. The second column provides the sequence identifier, "SEQ ID NO:X", for each contig sequence. The third column provides a unique contig identifier, "Contig ID:" for each contig sequence. The fourth column, provides a BAC identifier "BAC ID NO:A" for the BAC clone referenced in the corresponding row of the table. The fifth column provides the nucleotide sequence identifier, "SEQ ID NO:B" for a fragment of the BAC clone identified in column four of the corresponding row of the table. The sixth column, "Exon From-To", provides the location (i.e., nucleotide position numbers) within the polynucleotide sequence of SEQ ID NO:B which delineate certain polynucleotides of the invention that are also exemplary members of polynucleotide sequences that encode polypeptides of the invention (e.g., polypeptides containing amino acid sequences encoded by the polynucleotide sequences delineated in column six, and fragments and variants thereof).

TABLE 2

| Clone ID NO:Z | Contig ID: | SEQ ID NO:X | Analysis Method | PFam/NR Description | PFam/NR Accession Number | Score/ Percent Identity | NT From | NT To |
|------------------|---------------|-------------------|--------------------|--|-------------------------------|--|---|--|
| HDPTE21 | 1165861 | 11 | blastx.14 | (AB018414) Gab2 [Mus musculus] | gi 4589377 dbj BAA7 6738.1 | 74% 50% 55% 65% 68% 69% 66% 39% 32% 45% 36% 34% | 51 246 1650 1344 1620 1188 1260 1527 1017 1182 1528 2907 | 227 416 1784 1421 1667 1226 1295 1595 1100 1241 1584 2984 |
| HDPTE21 | 887711 | 443 | HMMER 2.1.1 | PFAM: PH domain | PF00169 | 25.2 | 31 | 129 |
| H6EDR51 | 930788 | 445 | HMMER 2.1.1 | PFAM: PH domain | PF00169 | 80.9 | 664 | 951 |
| | | | blastx.2 | (AF053974) SWAP-70 [Mus musculus] | gb AAC40155.1 | 53% 57% 26% 19% 43% 33% | 19 1291 1464 1566 1199 1214 | 996 1395 1760 1826 1279 1285 |
| HAPRA41 | 1154054 | 13 | blastx.14 | actin filament-associated protein [Gallus gallus] | gi 487418 gb AAA18 166.1 | 82% | 53 | 1261 |
| HAPRA41 | 926285 | 446 | HMMER 2.1.1 | PFAM: PH domain | PF00169 | 59.8 | 111 | 398 |

| | | | | | | | | |
|---------|---------|-----|-------------|--|-------------------------------------|-------------------|-------------------|---------------------|
| HBXBI07 | 954118 | 447 | blastx.2 | actin filament-associated protein [Gallus gallus] PFAM: PH domain | gb AAA18166.1 | 76% | 45 | 473 |
| | | | HMMER 2.1.1 | | PF00169 | 33.2 | 164 | 484 |
| | | | blastx.2 | (AF101054) PHR1 isoform 2 [Homo sapiens] | gb AAF18572.1 AF101054_1 | 100% 92% | 119 684 | 637 722 |
| HBXCM38 | 910086 | 15 | HMMER 1.8 | PFAM: Src homology domain 3 | PF00018 | 55.89 | 1062 | 1232 |
| | | | blastx.2 | unnamed protein product [unidentified] | emb CAB69447.1 | 92% 87% 77% | 402 13 1295 | 1316 396 1348 |
| HCE3E50 | 961098 | 448 | HMMER 1.8 | PFAM: PH (pleckstrin homology) domain | PF00169 | 50.5 | 146 | 448 |
| HCEQD04 | 1150868 | 17 | blastx.14 | (AF163255) adaptor protein DAPP1 [Mus musculus] | gi 5733602 gb AAD49698.1 AF163255_1 | 36% | 30 | 278 |
| HCEQD04 | 927873 | 449 | HMMER 2.1.1 | PFAM: PH domain | PF00169 | 44.9 | 139 | 258 |
| | | | blastx.2 | (AF163255) adaptor protein DAPP1 [Mus musculus] | gb AAD49698.1 AF163255_1 | 37% | 7 | 270 |
| HDPHI92 | 909900 | 18 | HMMER 2.1.1 | PFAM: RhoGAP domain | PF00620 | 235.1 | 888 | 1343 |
| | | | blastx.2 | racGAP [Dictyostelium discoideum] | emb CAA71241.1 | 37% | 825 | 1343 |
| HDPLT89 | 962403 | 19 | HMMER 2.1.1 | PFAM: Src homology domain 2 | PF00017 | 85.1 | 194 | 418 |
| | | | blastx.2 | (AF163254) adaptor protein DAPP1 [Homo sapiens] | gb AAD49697.1 AF163254_1 | 100% | 92 | 931 |
| HDPSU48 | 1228284 | 20 | blastx.14 | hypothetical protein | pir T13601 T13601 | 56% | 421 | 873 |

| | | | | 80H7.5 - fruit fly (Drosophila melanogaster) | | | 72% | 243 | 485 |
|---------|---------|-----|----------------------------|---|-------------------|--|-------|------|------|
| HDPSU48 | 909949 | 450 | HMMER 2.1.1 blastx.2 | PFAM: FYVE zinc finger | PF01363 | | 101.5 | 668 | 868 |
| | | | | (AL031027) /prediction=(method:""ge nefinder"", 1 1 1 PROTEIN)"", sp | emb CAA19842.1 | | 70% | 230 | 862 |
| HDPWE80 | 909916 | 21 | HMMER 2.1.1 blastx.2 | PFAM: PH domain | PF00169 | | 81.2 | 412 | 708 |
| | | | | (AF102854) membrane- associated guanylate kinase-interacting protein 2 Maguin-2 [Rattus norvegicus] | gb AAD04568.1 | | 36% | 349 | 756 |
| HDQFY84 | 971615 | 451 | HMMER 2.1.1 | PFAM: PH domain | PF00169 | | 52.1 | 1232 | 1507 |
| HEONQ19 | 930705 | 23 | HMMER 2.1.1 blastx.2 | PFAM: PH domain | PF00169 | | 42.5 | 213 | 533 |
| | | | | (AJ250425) Collybistin I [Rattus norvegicus] | emb CAB65966.1 | | 96% | 9 | 629 |
| HFCBB56 | 910073 | 24 | HMMER 1.8 blastx.2 | PFAM: EF hand | PF00036 | | 23.95 | 431 | 514 |
| | | | | 1-phosphatidylinositol- 4,5-bisphosphate phosphodiesterase 1 | pir S14113 S14113 | | 36% | 275 | 565 |
| HFKKZ94 | 926486 | 452 | HMMER 2.1.1 | PFAM: PH domain | PF00169 | | 55.3 | 226 | 558 |
| HHBGJ53 | 909912 | 453 | HMMER 2.1.1 | PFAM: PH domain | PF00169 | | 38.3 | 160 | 267 |
| HHFJF24 | 1212624 | 27 | blastx.14 | GUANINE | sp Q64096 DBS MO | | 83% | 3 | 566 |

| | | | | NUCLEOTIDE EXCHANGE FACTOR DBS (DBLS BIG SISTER) (MCF2 TRANSFORMING SEQUENCE-LIKE PROTEIN). | USE | 71% 79% 23% | 545 878 512 | 811 979 613 |
|---------|---------|-----|----------------------------|--|----------------------------------|-------------------|-------------------|-------------------|
| HHFJF24 | 910065 | 454 | HMMER 1.8 blastx.2 | PFAM: PH (pleckstrin homology) domain GUANINE NUCLEOTIDE EXCHANGE FACTOR DBS (DBL'S BIG SISTER) 1 (FRAGMENT). | PF00169 sp Q63406 DBS_RA T | 23.24 98% | 3 3 | 107 158 |
| HHFMM10 | 1178801 | 28 | blastx.14 | putative [Rattus norvegicus] | gi 397579 emb CAA5 2297.1 | 97% 91% | 138 503 | 263 613 |
| HHFMM10 | 962997 | 455 | HMMER 2.1.1 blastx.2 | PFAM: PH domain putative [Rattus norvegicus] | PF00169 emb CAA52297.1 | 42.9 95% | 251 131 | 487 493 |
| HHPBA42 | 901921 | 29 | HMMER 2.1.1 blastx.2 | PFAM: PH domain mitogen inducible gene mig-2 [Homo sapiens] | PF00169 emb CAA80852.1 | 42.4 61% | 352 1 | 663 822 |
| HHPSP89 | 910024 | 456 | HMMER 2.1.1 blastx.2 | PFAM: PH domain (AB023656) KIF1B-beta [Mus musculus] | PF00169 dbj BAA75243.1 | 62.3 87% | 562 118 | 855 906 |
| HKABX13 | 1167182 | 31 | blastx.14 | (AK000790) unnamed protein product [Homo sapiens] | gi 7021093 dbj BAA9 1379.1 | 98% 57% | 97 589 | 480 786 |

| | | | | | | | | |
|----------|---------|-----|----------------------------|---|------------------------------|-------|------|------|
| HKABX13 | 958656 | 457 | HMMER 1.8 blastx.2 | PFAM: PH (pleckstrin homology) domain (AK000790) unnamed protein product [Homo sapiens] | PF00169 dbj BAA91379.1 | 51.8 | 104 | 424 |
| HLTHG77 | 878592 | 458 | HMMER 2.1.1 blastx.2 | PFAM: PH domain (AK001472) unnamed protein product [Homo sapiens] | PF00169 dbj BAA91711.1 | 60.2 | 1254 | 1625 |
| HLWBZ09 | 957912 | 459 | HMMER 1.8 | PFAM: PH (pleckstrin homology) domain | PF00169 | 21.29 | 145 | 417 |
| HLWEH54 | 932133 | 460 | HMMER 2.1.1 | PFAM: PH domain | PF00169 | 114.1 | 556 | 849 |
| HL YAA41 | 1188029 | 35 | blastx.14 | SecG [Dictyostelium discoideum] | gi 1688318 gb AAB3 6958.1 | 43% | 173 | 352 |
| HL YAA41 | 909874 | 461 | HMMER 2.1.1 | PFAM: PH domain | PF00169 | 37.3 | 162 | 260 |
| HL YDV62 | 1154065 | 36 | blastx.14 | SecG [Dictyostelium discoideum] | gi 1688318 gb AAB3 6958.1 | 43% | 173 | 352 |
| HL YDV62 | 927872 | 462 | HMMER 2.1.1 blastx.2 | PFAM: PH domain (AC005496) unknown protein [Arabidopsis thaliana] | PF00169 gb AAC35236.1 | 58.6 | 188 | 406 |
| HMCFB47 | 910088 | 463 | HMMER 2.1.1 blastx.2 | PFAM: PH domain (AB005903) AtPH1 [Arabidopsis thaliana] | PF00169 dbj BAA84651.1 | 73 | 79 | 378 |
| HMSOI20 | 928168 | 464 | HMMER 1.8 | PFAM: PH (pleckstrin homology) domain | PF00169 | 30% | 85 | 375 |
| | | | | | | 18.44 | 154 | 384 |

| | | | | | | | | |
|---------|---------|-----|----------------------------|---|---|----------------------------------|-------------------------------|--------------------------------|
| HOENH55 | 1163460 | 39 | blastx.14 | p116Rip [Mus musculus] | gi 1657837 gb AAB18198.1 | 95% 86% 100% 80% 40% | 343 1 139 220 293 | 624 90 207 294 358 |
| HOENH55 | 922141 | 465 | HMMER 2.1.1 | PFAM: PH domain | PF00169 | 50.5 | 406 | 621 |
| HPIAI01 | 1078178 | 40 | blastx.2 blastx.14 | p116Rip [Mus musculus] unnamed protein product [unidentified] | gb AAB18198.1 gi 4756912 emb CAB42323.1 | 76% 36% 42% 72% | 1 213 414 183 | 624 437 476 215 |
| HPIAI01 | 909928 | 466 | HMMER 2.1.1 | PFAM: PH domain | PF00169 | 30.3 | 294 | 482 |
| HPJCT50 | 919836 | 467 | blastx.2 HMMER 2.1.1 | unnamed protein product [unidentified] PFAM: PH domain | emb CAB42187.1 PF00169 | 62% 81.4 | 10 728 | 195 1015 |
| HPMFE91 | 1164740 | 42 | blastx.2 blastx.14 | (AF210818) SWAP-70 [Homo sapiens] (AF136450) goodpasture antigen-binding protein [Homo sapiens] | gb AAF24486.1 AF210818_1 gi 4835895 gb AAD30288.1 AF136450_1 | 85% 89% 97% | 98 20 1097 | 1453 1129 1813 |
| HPMFE91 | 910026 | 468 | HMMER 2.1.1 | PFAM: PH domain | PF00169 | 81.9 | 332 | 613 |
| HRAED51 | 1090522 | 43 | blastx.2 blastx.14 | (AF136450) goodpasture antigen-binding protein [Homo sapiens] racGAP [Dictyostelium discoideum] | gb AAD30288.1 AF136450_1 gi 2190355 emb CAA71241.1 | 94% 40% 48% | 263 363 195 | 955 569 305 |
| HRAED51 | 909859 | 469 | HMMER 2.1.1 | PFAM: RhoGAP domain | PF00620 | 78.3 | 259 | 504 |

| | | | | | | | | |
|---------|---------|-----|-------------|--|---------------------------|---------------------------------|---------------------------------|-----------------------------------|
| | | | blastx.2 | beta-chimaerin [Rattus norvegicus] | gb AAA40809.1 | 28% | 259 | 585 |
| HSMBA19 | 924885 | 470 | HMMER 2.1.1 | PFAM: PH domain | PF00169 | 34.3 | 289 | 528 |
| | | | blastx.2 | (AL096767) dJ579N16.2 (SET binding factor 1) [Homo sapiens] | emb CAB63063.1 | 49% 76% | 4 533 | 531 607 |
| HSYCY88 | 914775 | 45 | HMMER 2.1.1 | PFAM: PH domain | PF00169 | 34.6 | 811 | 966 |
| | | | blastx.2 | putative [Rattus norvegicus] | emb CAA52297.1 | 97% 63% 88% 50% 44% | 607 21 425 962 1041 | 966 437 532 1111 1136 |
| HTEDW26 | 909749 | 46 | HMMER 2.1.1 | PFAM: FYVE zinc finger | PF01363 | 88.9 | 321 | 521 |
| | | | blastx.2 | (AF038388) actin-filament binding protein Frabin [Rattus norvegicus] | gb AAC27698.1 | 89% 51% | 57 1 | 959 81 |
| HTEKD92 | 1090524 | 47 | blastx.14 | (AK000074) unnamed protein product [Homo sapiens] | gi 7019925 dbj BAA90927.1 | 87% | 482 | 1165 |
| HTEKD92 | 910027 | 471 | HMMER 2.1.1 | PFAM: PH domain | PF00169 | 54.1 | 252 | 530 |
| | | | blastx.2 | (AK000074) unnamed protein product [Homo sapiens] | dbj BAA90927.1 | 87% | 468 | 1151 |
| HTLDT05 | 909752 | 472 | HMMER 2.1.1 | PFAM: PH domain | PF00169 | 36.9 | 59 | 271 |
| | | | blastx.2 | (AK000004) FLJ00004 protein [Homo sapiens] | dbj BAA92229.1 | 77% | 47 | 487 |

| | | | | | | | | |
|---------|---------|-----|----------------------------|--|-------------------------------|--|---|---|
| HTPDS90 | 529764 | 473 | HMMER 2.1.1 blastx.2 | PFAM: PH domain putative [Rattus norvegicus] | PF00169 emb CAA52297.1 | 65.3 79% 65% | 132 75 2 | 440 458 58 |
| HTPHM71 | 1194698 | 50 | blastx.14 | CDNA FLJ20260 FIS, CLONE COLF7627. | sp BAA91043 BAA9 1043 | 62% 70% 42% 59% 47% 23% 42% 80% 27% 38% | 61 1423 520 1192 700 889 1054 808 1552 600 | 348 1659 675 1287 762 1002 1131 837 1671 653 |
| HTPHM71 | 909878 | 474 | HMMER 1.8 blastx.2 | PFAM: PH (pleckstrin homology) domain (AK00267) unnamed protein product [Homo sapiens] | PF00169 dbj BAA91043.1 | 38.8 53% 31% 65% 32% 42% | 57 6 711 1139 550 957 | 341 341 929 1207 690 1034 |
| HUUAR12 | 944393 | 475 | HMMER 2.1.1 blastx.2 | PFAM: PH domain (AB008430) CDEP [Homo sapiens] | PF00169 dbj BAA24267.1 | 63.5 45% | 69 3 | 359 677 |
| HWAGP22 | 1150195 | 52 | blastx.14 | (AL031027) /prediction=(method:""ge nfinder"", 1 1 1 PROTEIN)"", sp | gi 3292902 emb CAA 19842.1 | 50% | 1653 | 1021 |
| HWAGP22 | 909919 | 476 | HMMER 2.1.1 blastx.2 | PFAM: FYVE zinc finger (AL031027) | PF01363 emb CAA19842.1 | 89.9 50% | 516 78 | 716 710 |

| | | | | /prediction=(method:""ge nefinder"" , 1 1 1 PROTEIN)"" , sp | | | | |
|---------|---------|-----|----------------|--|---|-------|------|------|
| HWBCE37 | 906968 | 53 | HMMER 1.8 | PFAM: PH (pleckstrin homology) domain | PF00169 | 60.73 | 39 | 353 |
| | | | blastx.2 | brain beta spectrin [Mus musculus] | gb AAC42040.1 | 30% | 93 | 386 |
| HWLFB60 | 1223499 | 54 | blastx.14 | CG1513 PROTEIN. | sp Q9V5D4 Q9V5D4 | 64% | 1445 | 1924 |
| | | | | | | 72% | 1127 | 1459 |
| | | | | | | 66% | 2 | 355 |
| | | | | | | 33% | 1943 | 2218 |
| | | | | | | 52% | 518 | 580 |
| | | | | | | 24% | 1295 | 1393 |
| | | | | | | 38% | 89 | 142 |
| HWLFB60 | 910018 | 477 | HMMER 2.1.1 | PFAM: PH domain | PF00169 | 43 | 8 | 241 |
| | | | blastx.2 | (AF000195) Contains similarity to Pfam domain: PF00169 (PH), 1 | gb AAC24270.1 | 63% | 14 | 241 |
| | | | | | | 33% | 238 | 414 |
| HDPGS16 | 909833 | 478 | HMMER 1.8 | PFAM: Protein kinase C terminal domain | PF00433 | 57.51 | 287 | 445 |
| | | | blastx.2 | (AJ245709) Akt-3 protein [Homo sapiens] | emb CAB53537.1 | 100% | 236 | 460 |
| | | | | | | 100% | 3 | 116 |
| HDQDV69 | 937850 | 56 | HMMER 2.1.1 | PFAM: Eukaryotic protein kinase domain | PF00069 | 212.5 | 68 | 598 |
| | | | blastx.2 | (AF169035) protein kinase [Homo sapiens] | gb AAF12758.1 AF1 69035_1 | 98% | 68 | 829 |
| HE6BK63 | 1153879 | 57 | blastx.14 | (AF128625) CDC42- binding protein kinase beta [Homo sapiens] | gi 5006445 gb AAD3 7506.1 AF128625_1 | 99% | 6 | 767 |
| | | | | | | | | |
| HE6BK63 | 661045 | 480 | HMMER | PFAM: Protein kinase C | PF00433 | 21.1 | 679 | 765 |

| | | | | | | | | |
|---------|---------|-----|--------------|--|---|--------|------|------|
| | | | 2.1.1 | terminal domain | gb AAD37506.1 AF1 28625_1 | 97% | 589 | 1179 |
| | | | blastx.2 | (AF128625) CDC42- binding protein kinase beta [Homo sapiens] | | 99% | 101 | 595 |
| | | | | | | 23% | 862 | 1152 |
| | | | | | | 18% | 922 | 1140 |
| | | | | | | 25% | 937 | 1152 |
| | | | | | | 22% | 934 | 1170 |
| | | | | | | 22% | 904 | 1161 |
| HE6BK63 | 974253 | 481 | blastx.14 | (AF128625) CDC42- binding protein kinase beta [Homo sapiens] | gi 5006445 gb AAD3 7506.1 AF128625_1 | 99% | 2 | 328 |
| | | | | | | 66% | 357 | 500 |
| | | | | | | 100% | 502 | 570 |
| | | | | | | 22% | 137 | 325 |
| | | | | | | 100% | 330 | 362 |
| | | | | | | 55% | 325 | 378 |
| | | | | | | 32% | 242 | 325 |
| | | | | | | 53% | 523 | 561 |
| HEKDR14 | 974255 | 58 | HMMER 1.8 | PFAM: Eukaryotic protein kinase domain | PF00069 | 244.21 | 297 | 1097 |
| | | | blastx.2 | (AF128625) CDC42- binding protein kinase beta [Homo sapiens] | gb AAD37506.1 AF1 28625_1 | 98% | 72 | 1733 |
| | | | | | | 22% | 1572 | 1706 |
| HFPER82 | 1152249 | 59 | blastx.14 | (AC004877) sco-spondin- mucin-like; similar to P98167 1 sapiens] | gi 3638957 gb AAC3 6301.1 | 68% | 137 | 90 |
| | | | | | | 34% | 227 | 123 |
| | | | | | | 42% | 569 | 513 |
| | | | | | | 50% | 387 | 346 |
| | | | | | | 34% | 332 | 255 |
| | | | | | | 54% | 84 | 52 |
| HFPER82 | 909835 | 482 | HMMER 1.8 | PFAM: Protein kinase C terminal domain | PF00433 | 33.87 | 943 | 1047 |
| | | | blastx.2 | human protein kinase B [Homo sapiens] | emb CAA43372.1 | 89% | 943 | 1053 |
| HAAAO58 | 1091088 | 60 | blastx.14 | (AF097887) Chp [Rattus | gi 3806122 gb AAC6 | 100% | 75 | 260 |

| | | | | | | | | |
|---------|---------|-----|----------------------------|---|---|--------------------------|------------------------|-------------------------|
| HAAAO58 | 912622 | 483 | HMMER 2.1.1 blastx.2 | norvegicus] PFAM: Ras family | 9198.1] PF00071 | 85.9 | 75 | 365 |
| HADFK69 | 1091937 | 61 | blastx.14 | (AF097887) Chp [Rattus norvegicus] | gb AAC69198.1 | 98% | 75 | 467 |
| HADFK69 | 912850 | 484 | HMMER 1.8 blastx.2 | (AF229839) kappa B-ras 1 [Homo sapiens] PFAM: Ras family (contains ATP/GTP binding P-loop) | gi 7008402 gb AAF34 998.1 PF00071 | 91% 85.8 | 207 109 | 752 573 |
| HDPMO62 | 1152329 | 62 | blastx.14 | (AF229839) kappa B-ras 1 [Homo sapiens] rab-related GTP-binding protein [Homo sapiens] | gb AAF34998.1 gi 1491714 emb CAA 68227.1 | 90% 38% 64% 50% | 49 303 145 31 | 543 596 303 96 |
| HDPMO62 | 912722 | 485 | HMMER 1.8 blastx.2 | PFAM: Ras family (contains ATP/GTP binding P-loop) rab-related GTP-binding protein [Homo sapiens] | PF00071 emb CAA68227.1 | 132.39 54% 57% | 127 133 20 | 432 444 76 |
| HDPMO85 | 912837 | 486 | HMMER 1.8 blastx.2 | PFAM: Ras family (contains ATP/GTP binding P-loop) (AF229840) kappa B-ras 2 [Homo sapiens] | PF00071 gb AAF34999.1 | 75.28 92% | 162 147 | 668 719 |
| HDPUY72 | 966153 | 487 | HMMER 2.1.1 blastx.2 | PFAM: Ras family (AF112206) ras-related protein rab-14 [Homo sapiens] | PF00071 gb AAF17194.1 AF1 12206_1 | 325.7 100% | 815 851 | 207 219 |
| HDTJF87 | 1154640 | 65 | blastx.14 | GTP-binding protein | gi 409166 gb AAA34 | 96% | 99 | 254 |

| | | | | | | | | |
|---------|---------|-----|----------------------------|--|---|--------------------------|--------------------------|---------------------------|
| HDTJF87 | 907527 | 488 | HMMER 2.1.1 blastx.2 | [Volvox carteri] PFAM: Ras family | 253.1 PF00071 | 198.2 | 110 | 394 |
| HE8TB94 | 1178794 | 66 | blastx.14 | strong similarity to the YPT1 sub-family of RAS proteins [Caenorhabditis elegans] | gb AAB52431.1 | 97% 73% | 89 396 | 394 737 |
| HE8TB94 | 935935 | 489 | HMMER 2.1.1 blastx.2 | ras-like protein [Homo sapiens] PFAM: Ras family | gi 190881 gb AAA36 547.1 PF00071 | 78% 78% 236.3 | 527 507 529 | 1075 548 1104 |
| HE8UB55 | 912932 | 490 | HMMER 1.8 blastx.2 | ras-like protein [Homo sapiens] PFAM: Ras family (contains ATP/GTP binding P-loop) | gb AAA36547.1 PF00071 | 80% 271.56 | 523 197 | 1101 676 |
| HEBGA65 | 1178633 | 68 | blastx.14 | (AL049685) hypothetical protein [Homo sapiens] | emb CAB41256.1 | 89% | 185 | 688 |
| HEBGA65 | 912815 | 491 | HMMER 1.8 blastx.2 | Rab24 protein [Mus musculus] PFAM: Ras family (contains ATP/GTP binding P-loop) | gi 438164 emb CAA8 0472.1 PF00071 | 90% 94% 176.38 | 435 1076 451 | 860 1252 939 |
| HEGBB59 | 1197907 | 69 | blastx.14 | Rab24 protein [Mus musculus] RAS-LIKE PROTEIN RASD (TRANSFORMING PROTEIN P23). | emb CAA80472.1 sp P03967 RASD_DI CDI | 92% 47% 57% 53% | 442 671 497 944 | 1035 928 679 988 |
| HEGBB59 | 912601 | 492 | HMMER 1.8 | PFAM: Ras family (contains ATP/GTP) | PF00071 | 75.96 | 370 | 546 |

| | | | | | | binding P-loop) | | | | | | |
|---------|---------|-----|--|--|-----------|---|--|-------------------------------------|---------|---------|---------|--|
| | | | | | blastx.2 | ras protein [Suberites domuncula] | | emb CAA77070.1 | 53% | 364 | 594 | |
| HELHC48 | 956003 | 70 | | | HMMER 1.8 | PFAM: Ras family (contains ATP/GTP binding P-loop) | | PF00071 | 156.24 | 756 | 403 | |
| | | | | | blastx.2 | (AF106681) ras-related GTP-binding protein [Homo sapiens] | | gb AAD43034.1 | 96% 76% | 756 817 | 403 767 | |
| HEOQH90 | 1212646 | 71 | | | blastx.14 | GTPase Rab37. | | sp AAF67162 AAF67162 | 93% | 12 | 680 | |
| HEOQH90 | 907532 | 493 | | | HMMER 1.8 | PFAM: Ras family (contains ATP/GTP binding P-loop) | | PF00071 | 305.73 | 88 | 666 | |
| | | | | | blastx.2 | (AB027137) RAB-26 [Homo sapiens] | | dbj BAA84707.1 | 72% | 94 | 657 | |
| HFKHA18 | 1152242 | 72 | | | blastx.14 | (AF058807) GTP-binding protein rah [Bos taurus] | | gi 4587775 gb AAD25874.1 | 97% 95% | 94 427 | 426 690 | |
| HFKHA18 | 972414 | 494 | | | HMMER 1.8 | PFAM: Ras family (contains ATP/GTP binding P-loop) | | PF00071 | 142.21 | 91 | 408 | |
| | | | | | blastx.2 | (AF058807) GTP-binding protein rah [Bos taurus] | | gb AAD25874.1 | 97% 93% | 88 409 | 420 684 | |
| HFKMA10 | 964258 | 73 | | | HMMER 1.8 | PFAM: Ras family (contains ATP/GTP binding P-loop) | | PF00071 | 254.6 | 254 | 721 | |
| | | | | | blastx.2 | Rab22a protein [Canis familiaris] | | emb CAA80473.1 | 99% | 242 | 724 | |
| HHBFM91 | 1092116 | 74 | | | blastx.14 | (AF091035) GTP-binding protein RAB21 [Homo sapiens] | | gi 6002585 gb AAF00048.1 AF091035_1 | 100% | 3 | 479 | |

| | | | | | | | | |
|---------|---------|-----|----------------|---|-------------------------------|--------|-----|-----|
| HHBFM91 | 912832 | 495 | HMMER 1.8 | PFAM: Ras family (contains ATP/GTP binding P-loop) | PF00071 | 86.13 | 2 | 340 |
| | | | blastx.2 | (AF091035) GTP-binding protein RAB21 [Homo sapiens] | gb AAF00048.1 AF0 91035_1 | 97% | 2 | 316 |
| HIBBF63 | 912715 | 75 | HMMER 2.1.1 | PFAM: Ras family | PF00071 | 211.1 | 3 | 416 |
| | | | blastx.2 | (AB027137) RAB-26 [Homo sapiens] | dbj BAA84707.1 | 100% | 3 | 419 |
| HMCEI38 | 1134410 | 76 | blastx.14 | (AF081353) GTP-binding protein [Homo sapiens] | gi 3859936 gb AAC7 2918.1 | 81% | 229 | 594 |
| HMCEI38 | 912580 | 496 | HMMER 2.1.1 | PFAM: Ras family | PF00071 | 103.6 | 297 | 452 |
| | | | blastx.2 | (AF081353) GTP-binding protein [Homo sapiens] | gb AAC72918.1 | 81% | 228 | 593 |
| HMWJD68 | 1154790 | 77 | blastx.14 | (AK00254) unnamed protein product [Homo sapiens] | gi 7020212 dbj BAA9 1034.1 | 98% | 54 | 614 |
| HMWJD68 | 912628 | 497 | HMMER 2.1.1 | PFAM: Ras family | PF00071 | 231.3 | 113 | 685 |
| | | | blastx.2 | (AK00254) unnamed protein product [Homo sapiens] | dbj BAA91034.1 | 99% | 53 | 613 |
| HOEOL58 | 1078090 | 78 | blastx.14 | small GTP-binding protein Rab27b [Homo sapiens] | gi 5107835 gb AAC5 1194.2 | 100% | 102 | 338 |
| HOEOL58 | 912836 | 498 | HMMER 1.8 | PFAM: Ras family (contains ATP/GTP binding P-loop) | PF00071 | 150.75 | 3 | 407 |
| | | | blastx.2 | small GTP-binding | gb AAC51194.2 | 97% | 3 | 407 |

| | | | | | | | | |
|---------|---------|-----|-----------------------------------|---|---|---|--|---|
| HRACA51 | 1162856 | 79 | blastx.14 | protein Rab27b [Homo sapiens] rab4b [Canis familiaris] | gi 919 emb CAA39800.1 | 100% | 54 | 677 |
| HRACA51 | 912776 | 499 | HMMER 2.1.1 blastx.2 | PFAM: Ras family | PF00071 | 310.6 | 55 | 666 |
| HSHAV32 | 912812 | 500 | HMMER 1.8 blastx.2 | rab4b [Canis familiaris] PFAM: Ras family (contains ATP/GTP binding P-loop) | emb CAA39800.1 PF00071 | 100% 242.77 | 43 192 | 666 872 |
| HTPDE66 | 971281 | 81 | blastx.2 HMMER 1.8 blastx.2 | (AB034244) RAB23 protein [Homo sapiens] PFAM: Ras family (contains ATP/GTP binding P-loop) small GTP-binding protein [Oryctolagus cuniculus] | dbj BAA87324.1 PF00071 gb AAA31261.1 | 99% 73.53 100% 63% | 162 260 260 216 | 872 427 427 281 |
| HTPDV73 | 997659 | 82 | blastx.14 | N-methyl-D-aspartate receptor subunit [Rattus rattus] | gi 286238 dbj BAA02500.1 | 66% 30% 70% 71% 83% 85% 71% | 39 123 5 290 123 248 331 | 74 182 34 310 140 268 351 |
| HTPDV73 | 912947 | 501 | HMMER 1.8 blastx.2 | PFAM: Ras family (contains ATP/GTP binding P-loop) (AL049685) hypothetical protein [Homo sapiens] | PF00071 emb CAB41256.1 | 205.32 97% | 306 312 | 740 746 |
| HTPHE33 | 963658 | 502 | HMMER | PFAM: Ras family | PF00071 | 94.19 | 993 | 1433 |

| | | | 1.8 | (contains ATP/GTP binding P-loop) | | | | |
|---------|---------|-----|-------------|---|--------------------------|-------------------|-------------------|-------------------|
| | | | blastx.2 | (AF095350) RAB-like protein 2A [Homo sapiens] | gb AAD51377.1 AF095350_1 | 83% 93% | 993 793 | 1478 1014 |
| HUFDN58 | 1224609 | 84 | blastx.14 | RAS-LIKE PROTEIN RASD (TRANSFORMING PROTEIN P23). | sp P03967 RASD_DI CDI | 47% 57% 53% | 664 490 937 | 921 672 981 |
| HUFDN58 | 912929 | 503 | HMMER 2.1.1 | PFAM: Ras family | PF00071 | 80.7 | 42 | 296 |
| | | | blastx.2 | ras-related protein [Dictyostelium discoideum] | emb CAA78508.1 | 43% | 3 | 299 |
| HUVFX92 | 1225329 | 85 | blastx.14 | GTP-binding protein ypt1 [similarity] - Neurospora crassa | pir S30096 S30096 | 88% | 54 | 308 |
| HUVFX92 | 912672 | 504 | HMMER 2.1.1 | PFAM: Ras family | PF00071 | 161 | 81 | 278 |
| | | | blastx.2 | (AF101310) similar to RAS-related proteins; contains similarity 1 | gb AAC69218.1 | 100% | 54 | 275 |
| HWAEG71 | 1182321 | 86 | blastx.14 | rab-related GTP-binding protein [Rattus norvegicus] | gi 206543 gb AAA42000.1 | 96% | 85 | 690 |
| HWAEG71 | 931547 | 505 | HMMER 1.8 | PFAM: Ras family (contains ATP/GTP binding P-loop) | PF00071 | 147.95 | 116 | 475 |
| | | | blastx.2 | rab-related GTP-binding protein [Rattus norvegicus] | gb AAA42000.1 | 98% 80% | 86 477 | 493 569 |

| | | | | | | | | |
|---------|---------|-----|----------------|--|-----------------------------|--------------------------|------------------------|--------------------------|
| HWAHD49 | 1228064 | 87 | blastx.14 | GTP-BINDING PROTEIN RAH (FRAGMENT). | sp Q9XS71 Q9XS71 | 97% 94% | 391 742 | 747 1011 |
| HWAHD49 | 972413 | 506 | HMMER 1.8 | PFAM: Ras family (contains ATP/GTP binding P-loop) | PF00071 | 143.42 | 394 | 717 |
| | | | blastx.2 | LMW G-protein=low- molecular-weight GTP- binding protein [mice, HT4 neural cell line, Peptide, 208 aa] [Mus sp.] | gb AAB20669.1 | 95% 76% | 391 726 | 720 764 |
| HWLGG31 | 1178825 | 88 | blastx.14 | RAB15 [Rattus norvegicus] | gj 206537 gb AAA41 995.1 | 92% | 81 | 716 |
| HWLGG31 | 912581 | 507 | HMMER 2.1.1 | PFAM: Ras family | PF00071 | 301.8 | 98 | 562 |
| | | | blastx.2 | RAB15 [Rattus norvegicus] | gb AAA41995.1 | 90% | 71 | 562 |
| HWLKF25 | 912842 | 508 | HMMER 2.1.1 | PFAM: Ras family | PF00071 | 298.2 | 311 | 889 |
| | | | blastx.2 | (AB036693) RAB9-like protein [Homo sapiens] | dbj BAA89542.1 | 100% | 287 | 889 |
| H2CBH45 | 963811 | 90 | HMMER 1.8 | PFAM: Src homology domain 3 | PF00018 | 13 | 194 | 310 |
| | | | blastx.2 | Kryn [Mus musculus] | dbj BAA19686.1 | 85% 79% 87% 70% | 2 381 460 131 | 373 467 483 160 |
| HAGDN53 | 895963 | 509 | HMMER 1.8 | PFAM: Src homology domain 3 | PF00018 | 22.95 | 270 | 335 |
| | | | blastx.2 | coded for by C. elegans cDNA yk34a9.5; coded | gb AAA96115.1 | 43% 38% | 165 103 | 455 156 |

| | | | | | | | | |
|---------|---------|-----|----------------------------|--|--|---------------------------|-------------------------|--------------------------|
| HAMFM39 | 971347 | 92 | HMMER 1.8 blastx.2 | for by <i>C. elegans</i> 1 elegans] PFAM: Src homology domain 3 (AK001509) unnamed protein product [Homo sapiens] PFAM: SH3 domain | PF00018 dbj BAA91729.1 PF00018 | 67.14 59% 68.5 | 1136 4511 615 | 1306 4017 785 |
| HBGQT03 | 908173 | 93 | HMMER 2.1.1 blastx.2 | (AF130979) SH3 domain- containing protein 6511 [Homo sapiens] ferrienterobactin receptor precursor [Escherichia coli] PFAM: Src homology domain 3 | gb AAF04472.1 AF1 30979_1 gi 1778500 gb AAB4 0783.1 PF00018 | 93% 93% 4.07 | 3 729 445 | 791 1 510 |
| HBGSJ13 | 1150790 | 94 | blastx.14 | ferrienterobactin receptor precursor [Escherichia coli] PFAM: SH3 domain | PF00018 | 92% 49.7 | 64 212 | 684 376 |
| HBGSJ13 | 878322 | 510 | HMMER 1.8 blastx.2 | p115 [Homo sapiens] PFAM: Src homology domain 3 PFAM: Src homology domain 3 | emb CAA55394.1 PF00018 PF00018 | 41% 53.06 4.22 | 14 392 33 | 397 568 62 |
| HBIBQ89 | 909782 | 95 | HMMER 2.1.1 blastx.2 | (AF039571) peripheral benzodiazepine receptor interacting protein; PBR- IP/PRAX1 [Homo sapiens] PFAM: SH3 domain | gi 4104812 gb AAD1 1957.1 PF00018 | 96% 74% 100% 52% | 45 702 887 381 | 629 887 979 500 |
| HCECM90 | 945088 | 96 | HMMER 1.8 blastx.2 | | | | | |
| HCEPH71 | 522739 | 97 | HMMER 1.8 blastx.14 | | | | | |
| HCFMT57 | 1175204 | 98 | | | | | | |

| | | | | | | | | | | | |
|---------|---------|-----|--------------|---|----------|-----------------------------|-------|-----|-----|------|------|
| | | | | | sapiens] | | | | 44% | 381 | 461 |
| | | | | | | | | | 55% | 327 | 386 |
| | | | | | | | | | 28% | 161 | 319 |
| | | | | | | | | | 50% | 744 | 803 |
| | | | | | | | | | 58% | 780 | 830 |
| | | | | | | | | | 35% | 160 | 243 |
| | | | | | | | | | 34% | 1693 | 1770 |
| | | | | | | | | | 47% | 468 | 518 |
| | | | | | | | | | 55% | 190 | 243 |
| | | | | | | | | | 58% | 795 | 830 |
| | | | | | | | | | 42% | 622 | 684 |
| | | | | | | | | | 29% | 73 | 153 |
| | | | | | | | | | 42% | 607 | 663 |
| | | | | | | | | | 35% | 54 | 137 |
| | | | | | | | | | 36% | 643 | 717 |
| | | | | | | | | | 31% | 631 | 717 |
| | | | | | | | | | 25% | 136 | 231 |
| | | | | | | | | | 38% | 111 | 188 |
| | | | | | | | | | 28% | 114 | 230 |
| | | | | | | | | | 28% | 144 | 227 |
| HCFMT57 | 765375 | 511 | HMMER 1.8 | PFAM: Src homology domain 3 | | PF00018 | 14.55 | 107 | 3 | | |
| | | | blastx.2 | (AF039571) peripheral benzodiazepine receptor interacting protein; PBR- IP/PRAX1 [Homo sapiens] | | gb AAD11957.1 | 96% | 377 | 3 | | |
| HCOMM05 | 1173146 | 99 | blastx.14 | epidermal growth factor receptor kinase substrate [Homo sapiens] | | gi 530823 gb AAA62 280.1 | 44% | 456 | 722 | | |
| | | | | | | | 59% | 189 | 371 | | |
| | | | | | | | 46% | 723 | 851 | | |
| | | | | | | | 23% | 54 | 233 | | |
| | | | | | | | 36% | 126 | 191 | | |

| | | | | | | | | |
|---------|--------|-----|----------------------------|---|---|-----------------------------------|---------------------------------|----------------------------------|
| HCOMM05 | 925952 | 512 | HMMER 1.8 blastx.2 | PFAM: Src homology domain 3 epidermal growth factor receptor kinase substrate [Homo sapiens] | PF00018 gb AAA62280.1 | 63% 59.48 46% 43% 23% | 1081 178 445 115 43 | 1113 342 840 435 222 |
| HCOOZ11 | 965306 | 100 | HMMER 1.8 blastx.2 | PFAM: Src homology domain 3 (AL022238) dJ1042K10.2 (supported by GENSCAN, FGENES and GENEWISE) [Homo sapiens] | PF00018 emb CAA18266.1 | 5.22 100% | 179 182 | 214 589 |
| HCWFF88 | 506577 | 101 | HMMER 1.8 | PFAM: Src homology domain 3 | PF00018 | 4.92 | 140 | 181 |
| HDMAV01 | 911386 | 513 | HMMER 1.8 blastx.2 | PFAM: Src homology domain 3 unnamed protein product [unidentified] | PF00018 emb CAB42388.1 | 52.13 73% 100% | 264 111 3 | 413 410 116 |
| HDPDA47 | 929193 | 103 | HMMER 1.8 blastx.2 | PFAM: Src homology domain 3 (AL049683) hypothetical protein [Homo sapiens] | PF00018 emb CAB41255.1 | 12.52 69% 53% | 691 145 945 | 810 1026 1022 |
| HDPFF24 | 909232 | 104 | HMMER 2.1.1 blastx.2 | PFAM: KRAB box (AC007228) R31665_2 [AA 1-673] [Homo sapiens] | PF01352 gb AAD23606.1 AC0 07228_1 | 121.3 50% | 158 158 | 349 457 |
| HDPPO35 | 966248 | 105 | HMMER 1.8 blastx.2 | PFAM: Src homology domain 3 (AL049683) hypothetical | PF00018 emb CAB41255.1 | 14.07 39% | 600 84 | 749 1148 |

| | | | | | | | | |
|---------|---------|-----|--------------------------|--|---|---|---|---|
| HDPSR74 | 911396 | 106 | HMMER 1.8 blastx.2 | protein [Homo sapiens] PFAM: Src homology domain 3 (AF104246) enhancer of filamentation 1 homolog [Gallus gallus] | PF00018 gb AAD11795.1 | 47.19 48% | 293 281 | 460 553 |
| HDTKQ14 | 886936 | 107 | HMMER 1.8 blastx.2 | PFAM: Src homology domain 3 (AL049683) hypothetical protein [Homo sapiens] | PF00018 emb CAB41255.1 | 12.87 100% 56% | 430 439 76 | 546 555 291 |
| HE6GF02 | 1150897 | 108 | blastx.14 | (AJ007012) Fish protein [Mus musculus] | gi 3702174 emb CAA 07416.1 | 75% 66% 70% 39% 40% 38% 39% 41% 38% 37% 37% 50% 54% | 795 603 189 603 804 792 795 600 582 552 150 532 459 | 613 427 70 430 613 637 637 427 433 481 70 485 427 |
| HE6GF02 | 911263 | 514 | HMMER 1.8 blastx.2 | PFAM: Src homology domain 3 (AJ007012) Fish protein [Mus musculus] | PF00018 emb CAA07416.1 | 51.15 77% 44% | 10 10 201 | 174 186 275 |
| HE8PK12 | 909884 | 109 | HMMER 1.8 blastx.2 | PFAM: Src homology domain 3 (AF136380) SH3P12 protein [Homo sapiens] | PF00018 gb AAD27647.1 AF1 36380_1 | 58.12 82% | 197 59 | 361 367 |
| HE9SE62 | 911476 | 110 | HMMER | PFAM: Src homology | PF00018 | 47.65 | 268 | 435 |

| | | | | | | | | | | |
|--|--|-----|--------|----------------|--|----------------|------------|--------------|-------------|--|
| | | | | | domain 3 | | | | | |
| | | | | blastx.2 | (AK000007) FLJ00007 protein [Homo sapiens] | dbj BAA92232.1 | 43% 64% | 4 877 | 435 927 | |
| | | 515 | 968826 | HMMER 1.8 | PFAM: Src homology domain 3 | PF00018 | 79.81 | 316 | 483 | |
| | | | | blastx.2 | (AL049758) dJ437M21.3 (protein kinase C and casein kinase substrate in neurons 2) [Homo sapiens] | emb CAB51395.1 | 99% | 178 | 486 | |
| | | 112 | 911264 | HMMER 2.1.1 | PFAM: SH3 domain | PF00018 | 78.6 | 105 | 269 | |
| | | | | blastx.2 | (AF030131) Plenty of SH3s; POSH [Mus musculus] | gb AAC40070.1 | 78% | 3 | 473 | |
| | | 113 | 657020 | HMMER 1.8 | PFAM: Src homology domain 3 | PF00018 | 4.85 | 168 | 203 | |
| | | 114 | 932851 | HMMER 1.8 | PFAM: Src homology domain 3 | PF00018 | 30.41 | 526 | 708 | |
| | | 115 | 965304 | HMMER 2.1.1 | PFAM: TBC domain | PF00566 | 179.1 | 2305 | 1655 | |
| | | | | blastx.2 | (AL022238) dJ1042K10.2 (supported by GENSCAN, FGENES and GENEWISE) [Homo sapiens] | emb CAA18266.1 | 97% 98% | 2635 1276 | 1268 389 | |
| | | 116 | 935932 | HMMER 2.1.1 | PFAM: RhoGEF domain | PF00621 | 51.3 | 229 | 486 | |
| | | | | blastx.2 | (AJ250425) Collybistin I [Rattus norvegicus] | emb CAB65966.1 | 96% | 1 | 483 | |
| | | 117 | 839777 | HMMER | PFAM: Src homology | PF00018 | 3.85 | 342 | 419 | |

| | | | | | | | | |
|----------|--------|-----|--------------|---|--------------------------|---------------------------------|---------------------------|---------------------------------|
| | | | 1.8 | domain 3 (AK000579) unnamed protein product [Homo sapiens] | dbj BAA91269.1 | 98% | 252 | 458 |
| HLWFN63 | 908437 | 118 | HMMER 1.8 | PFAM: Src homology domain 3 | PF00018 | 12.81 | 515 | 664 |
| | | | blastx.2 | (AL049683) hypothetical protein [Homo sapiens] | emb CAB41255.1 | 44% | 464 | 1024 |
| HMEFT66 | 856149 | 119 | HMMER 1.8 | PFAM: Src homology domain 3 | PF00018 | 28.51 | 5 | 136 |
| HMSCD15 | 918133 | 120 | HMMER 1.8 | PFAM: Src homology domain 3 | PF00018 | 41.06 | 453 | 599 |
| | | | blastx.2 | (AK000975) unnamed protein product [Homo sapiens] | dbj BAA91451.1 | 98% 29% 28% | 453 387 80 | 635 479 175 |
| HMSHO64 | 746582 | 121 | HMMER 1.8 | PFAM: Src homology domain 3 | PF00018 | 11.08 | 316 | 405 |
| | | | blastx.2 | (AF030131) Plenty of SH3s; POSH [Mus musculus] | gb AAC40070.1 | 47% | 1 | 411 |
| HMTAW83 | 911385 | 122 | HMMER 1.8 | PFAM: Src homology domain 3 | PF00018 | 76.18 | 1 | 159 |
| | | | blastx.2 | (AF230904) c-Cbl-interacting protein [Homo sapiens] | gb AAF37854.1 AF230904_1 | 94% 52% 48% 61% 75% | 1 7 7 298 425 | 354 210 168 351 460 |
| HMOVAM09 | 963814 | 123 | HMMER 1.8 | PFAM: Src homology domain 3 | PF00018 | 4.79 | 728 | 802 |
| | | | blastx.2 | (AK001580) unnamed protein product [Homo sapiens] | dbj BAA91769.1 | 96% | 20 | 802 |

| | | | | | | | | |
|---------|---------|-----|----------------------------|--|---|------------|-----------|------------|
| HNSAA28 | 946988 | 124 | HMMER 2.1.1 blastx.2 | sapiens] PFAM: SH3 domain | PF00018 | 149 | 757 | 915 |
| | | | | (AF146277) adapter protein CMS [Homo sapiens] | gb AAD34595.1 AF1 46277_1 | 82% | 4 | 1554 |
| HNSAA28 | 972348 | 516 | blastx.14 | (AF146277) adapter protein CMS [Homo sapiens] | gi 4960047 gb AAD3 4595.1 AF146277_1 | 88% | 21 | 449 |
| HOGEQ43 | 935465 | 517 | HMMER 1.8 blastx.2 | PFAM: Src homology domain 3 | PF00018 | 28.13 | 58 | 132 |
| | | | | (AF132480) Ese2 protein [Mus musculus] | gb AAD19748.1 | 93% | 37 | 132 |
| HOUDH19 | 1150918 | 126 | blastx.14 | (AC007842) BC331191_1 [Homo sapiens] | gi 5080758 gb AAD3 9268.1 AC007842_3 | 91% | 350 | 27 |
| HOUDH19 | 908588 | 518 | HMMER 2.1.1 blastx.2 | PFAM: KRAB box | PF01352 | 169.7 | 241 | 429 |
| | | | | (AC007842) BC331191_1 [Homo sapiens] | gb AAD39268.1 AC0 07842_3 | 91% | 226 | 549 |
| HOUFT36 | 911293 | 127 | HMMER 2.1.1 blastx.2 | PFAM: PDZ domain (Also known as DHR or GLGF). | PF00595 | 35.3 | 322 | 558 |
| | | | | (AF162130) MAGUK protein TEM-61 [Homo sapiens] | gb AAD45919.2 AF1 62130_1 | 91% 98% | 196 23 | 846 193 |
| HPMFL08 | 959569 | 128 | HMMER 1.8 blastx.2 | PFAM: Src homology domain 3 | PF00018 | 4.97 | 209 | 238 |
| HRSMD49 | 723025 | 129 | HMMER 1.8 blastx.2 | PFAM: Src homology domain 3 | PF00018 | 4.76 | 199 | 270 |
| HSDII69 | 917180 | 130 | HMMER 1.8 blastx.2 | PFAM: Src homology domain 3 | PF00018 | 4.09 | 382 | 429 |

| | | | | | | | | |
|---------|--------|-----|----------------------------|---|---|---------------------|----------------|-------------------|
| HSDSB06 | 949151 | 131 | HMMER 2.1.1 blastx.2 | PFAM: SH3 domain (AL133047) hypothetical protein [Homo sapiens] | PF00018 | 249.3 | 483 | 647 |
| | | | | | emb CAB61374.1 | 98% 30% 33% | 3 6 222 | 863 848 848 |
| HSFAM09 | 573345 | 519 | HMMER 1.8 | PFAM: Src homology domain 3 | PF00018 | 5.33 | 195 | 218 |
| HSSAX53 | 507509 | 133 | HMMER 1.8 | PFAM: Src homology domain 3 | PF00018 | 4.36 | 266 | 331 |
| HSVAW49 | 689674 | 520 | HMMER 1.8 blastx.2 | PFAM: Src homology domain 3 (AF146277) adapter protein CMS [Homo sapiens] | PF00018 gb AAD34595.1 AF1 46277_1 | 36.33 97% | 77 65 | 169 166 |
| HTEAG49 | 954614 | 135 | HMMER 1.8 | PFAM: Src homology domain 3 | PF00018 | 4.51 | 312 | 238 |
| HTLBH67 | 751985 | 136 | HMMER 1.8 | PFAM: Src homology domain 3 | PF00018 | 37.78 | 16 | 162 |
| HTLJC71 | 922923 | 137 | HMMER 1.8 blastx.2 | PFAM: Src homology domain 3 (AL133030) hypothetical protein [Homo sapiens] | PF00018 emb CAB61362.1 | 9.14 94% | 1152 3 | 1340 1355 |
| HTPAD46 | 503313 | 138 | HMMER 1.8 | PFAM: Src homology domain 3 | PF00018 | 4.14 | 160 | 186 |
| HTTKP07 | 911390 | 139 | HMMER 1.8 blastx.2 | PFAM: Src homology domain 3 (AL049683) hypothetical protein [Homo sapiens] | PF00018 emb CAB41255.1 | 15.82 51% 56% | 47 8 292 | 196 289 450 |
| HUCOW17 | 933357 | 140 | HMMER 1.8 blastx.2 | PFAM: Src homology domain 3 Graf protein [Homo] | PF00018 emb CAA71414.2 | 20.28 67% | 647 1 | 739 261 |

| | | | | | | | | |
|---------|---------|-----|--------------|--|-------------------------------|-------|-----|-----|
| HWHGF52 | 726102 | 141 | HMMER 1.8 | sapiens] | PF00018 | 50% | 608 | 751 |
| | | | blastx.2 | PFAM: Src homology domain 3 | | | | |
| HWHHB69 | 690442 | 521 | HMMER 1.8 | PFAM: Src homology domain 3 | gb AAB33461.1 | 74% | 3 | 203 |
| | | | blastx.2 | DBS=Dbl guanine nucleotide exchange factor homolog [mice, 32D 1 | | | | |
| HWLFH94 | 1151387 | 143 | HMMER 1.8 | PFAM: Src homology domain 3 | gb AAF35985.1 AF1 78432 1 | 70% | 91 | 315 |
| | | | blastx.2 | (AF178432) SH3 protein [Homo sapiens] | | | | |
| HWLFH94 | 909682 | 522 | HMMER 1.8 | PFAM: Src homology domain 3 | gi 7020230 dbj BAA9 1041.1 | 41% | 545 | 345 |
| | | | blastx.2 | (AK000265) unnamed protein product [Homo sapiens] | | | | |
| HWMBM13 | 909683 | 144 | HMMER 1.8 | PFAM: Src homology domain 3 | dbj BAA91041.1 | 40% | 215 | 535 |
| | | | blastx.2 | (AK000265) unnamed protein product [Homo sapiens] | | | | |
| HWWDN34 | 911357 | 145 | HMMER 1.8 | PFAM: Src homology domain 3 | gb AAA16358.1 | 35% | 33 | 317 |
| | | | blastx.2 | Eps8 [Mus musculus] | | | | |
| HCEML27 | 771667 | 523 | HMMER 1.8 | PFAM: Src homology domain 3 | gb AAC40124.1 | 42% | 56 | 874 |
| | | | blastx.2 | (AF053130) unconventional myosin MYO15 [Mus musculus] | | | | |
| HCEML27 | 771667 | 523 | HMMER 1.8 | PFAM: Src homology domain 3 | PF00017 | 42.63 | 14 | 202 |
| | | | blastx.2 | PFAM: Src homology domain 3 | | | | |

| | | | 1.8 | domain 2 | | | | |
|---------|---------|-----|-------------|---|-------------------------------------|--|---------------------------------------|---|
| HELHJ69 | 1128924 | 147 | blastx.2 | (AL049924) hypothetical protein [Homo sapiens] | emb CAB43208.1 | 88% | 2 | 322 |
| | | | blastx.14 | (AF124251) SH2-containing protein Nsp3 [Homo sapiens] | gi 4704739 gb AAD28246.1 AF124251_1 | 81% 76% 52% 60% 63% | 66 586 590 55 612 | 593 624 640 99 644 |
| HELHJ69 | 911262 | 524 | HMMER 1.8 | PFAM: Src homology domain 2 | PF00017 | 72.59 | 241 | 483 |
| | | | blastx.2 | (AF124251) SH2-containing protein Nsp3 [Homo sapiens] | gb AAD28246.1 AF124251_1 | 78% 76% 60% | 67 587 56 | 645 625 100 |
| HFKLA09 | 952634 | 525 | HMMER 2.1.1 | PFAM: Src homology domain 2 | PF00017 | 46.9 | 758 | 1036 |
| HSBBF79 | 965764 | 149 | HMMER 1.8 | PFAM: Src homology domain 2 | PF00017 | 69.47 | 384 | 614 |
| HSLKA77 | 911589 | 526 | HMMER 1.8 | PFAM: Src homology domain 2 | PF00017 | 37.25 | 301 | 405 |
| | | | blastx.2 | tensin [Gallus gallus] | gb AAA49087.1 | 58% 51% 31% | 178 29 3 | 432 115 155 |
| hagdr21 | 1090433 | 151 | blastx.14 | p66shc [Homo sapiens] | gi 1899055 gb AAB49972.1 | 69% 72% 59% 37% 35% 34% | 848 134 380 665 72 701 | 1150 412 475 751 164 778 |
| hagdr21 | 1002124 | 527 | blastx.14 | MUS p66 Shc [Mus musculus] | gi 1200456 gb AAA91777.1 | 91% | 62 | 268 |
| HHFNH27 | 1025277 | 152 | blastx.2 | collagen alpha 1(III) chain | pir S05272 CGHU7L | 30% | 89 | 1609 |

| | | | | precursor - human | | | | |
|-----|------|------|--|-------------------|--|--|--|--|
| 28% | 53 | 1606 | | | | | | |
| 30% | 1061 | 1741 | | | | | | |
| 32% | 1094 | 1606 | | | | | | |
| 32% | 956 | 1741 | | | | | | |
| 32% | 1094 | 1606 | | | | | | |
| 31% | 851 | 1735 | | | | | | |
| 30% | 830 | 1741 | | | | | | |
| 30% | 1073 | 1618 | | | | | | |
| 28% | 1094 | 1831 | | | | | | |
| 28% | 1022 | 1735 | | | | | | |
| 30% | 1088 | 1741 | | | | | | |
| 30% | 21 | 593 | | | | | | |
| 30% | 89 | 655 | | | | | | |
| 34% | 86 | 910 | | | | | | |
| 28% | 18 | 593 | | | | | | |
| 27% | 27 | 455 | | | | | | |
| 32% | 128 | 655 | | | | | | |
| 30% | 80 | 601 | | | | | | |
| 34% | 27 | 257 | | | | | | |
| 30% | 42 | 599 | | | | | | |
| 28% | 53 | 541 | | | | | | |
| 34% | 21 | 257 | | | | | | |
| 28% | 33 | 455 | | | | | | |
| 35% | 12 | 257 | | | | | | |
| 33% | 9 | 269 | | | | | | |
| 28% | 36 | 593 | | | | | | |
| 36% | 21 | 245 | | | | | | |
| 28% | 21 | 386 | | | | | | |
| 30% | 9 | 593 | | | | | | |
| 27% | 67 | 477 | | | | | | |
| 30% | 37 | 477 | | | | | | |
| 29% | 1746 | 289 | | | | | | |

| | | | | | | | | |
|---------|---------|-----|-----------|--|--------------------------|-----|------|------|
| HTLIT05 | 1217625 | 153 | blastx.14 | CDNA FLJ10243 FIS, CLONE HEMBB1000631, WEAKLY SIMILAR TO 1 | sp BAA91505 BAA9 1505 | 31% | 1656 | 835 |
| | | | | | | 32% | 1848 | 952 |
| | | | | | | 29% | 1662 | 955 |
| | | | | | | 36% | 525 | 55 |
| | | | | | | 37% | 525 | 19 |
| | | | | | | 32% | 525 | 37 |
| | | | | | | 33% | 1659 | 1063 |
| | | | | | | 30% | 1656 | 1021 |
| | | | | | | 30% | 1644 | 958 |
| | | | | | | 32% | 642 | 64 |
| | | | | | | 34% | 534 | 85 |
| | | | | | | 33% | 592 | 11 |
| | | | | | | 30% | 654 | 7 |
| | | | | | | 39% | 226 | 8 |
| | | | | | | 28% | 598 | 2 |
| | | | | | | 30% | 648 | 85 |
| | | | | | | 41% | 229 | 11 |
| | | | | | | 30% | 589 | 17 |
| | | | | | | 37% | 211 | 11 |
| | | | | | | 34% | 226 | 23 |
| | | | | | | 33% | 250 | 11 |
| | | | | | | 35% | 226 | 23 |
| | | | | | | 43% | 190 | 11 |
| | | | | | | 36% | 259 | 41 |
| | | | | | | 44% | 125 | 45 |
| | | | | | | 52% | 128 | 72 |
| HTLIT05 | 1095161 | 528 | blastx.14 | (AK001105) unnamed | gi 7022161 dbj BAA9 | 49% | 212 | 577 |

| | | | | | protein product [Homo sapiens] | 1505.1 | | | |
|---------|---------|-----|-------------|--|---|---------------------------|--------|-----|-----|
| HAPNV33 | 1151374 | 154 | blastx.14 | | (AK001267) unnamed protein product [Homo sapiens] | gi 7022415 dbj BAA91590.1 | 100% | 1 | 774 |
| HAPNV33 | 947872 | 529 | HMMER 1.8 | | PFAM: ATPases associated with various cellular activities (AAA) | PF00004 | 120.31 | 61 | 450 |
| | | | blastx.14 | | (AF016427) Contains similarity to Pfam domain: 1 elegans] | gi 2291232 gb AAB65351.1 | 53% | 1 | 447 |
| HBTA84 | 1128800 | 155 | blastx.14 | | ATP-dependent Clp protease ATP-binding subunit ClpA. [Escherichia coli] | gi 1651401 dbj BAA35601.1 | 100% | 3 | 299 |
| HBTA84 | 781946 | 530 | HMMER 1.8 | | PFAM: ATPases associated with various cellular activities (AAA) | PF00004 | 20.81 | 122 | 232 |
| HDPVY89 | 827026 | 156 | HMMER 2.1.1 | | PFAM: ATPases associated with various cellular activities (AAA) | PF00004 | 30.6 | 431 | 490 |
| HGLDB21 | 455474 | 531 | HMMER 1.8 | | PFAM: ATPases associated with various cellular activities (AAA) | PF00004 | 19.89 | 12 | 80 |
| HMIAN37 | 947881 | 158 | HMMER 2.1.1 | | PFAM: ATPases associated with various cellular activities (AAA) | PF00004 | 109 | 436 | 642 |
| | | | blastx.2 | | Similarity to Yeast MSP1 protein (TAT-binding homolog 4) (SW:MSP1_YEAST) [Caenorhabditis elegans] | emb CAA93516.1 | 45% | 91 | 642 |

| | | | | | | | | |
|---------|---------|-----|--------------|--|---|--------------------------|----------------------|-------------------------|
| HODAK55 | 745332 | 532 | HMMER 1.8 | PFAM: ATPases associated with various cellular activities (AAA) | PF00004 | 60.69 | 11 | 157 |
| HSLEI59 | 1128801 | 160 | blastx.14 | ATP-dependent Clp protease ATP-binding subunit ClpA. [Escherichia coli] | gi 1651401 dbj BAA3 5601.1 | 94% | 3 | 770 |
| HSLEI59 | 781945 | 533 | HMMER 1.8 | PFAM: ATPases associated with various cellular activities (AAA) | PF00004 | 20.14 | 96 | 206 |
| HSQFH29 | 1217061 | 161 | blastx.14 | SPAF. | sp Q9Z2K7 Q9Z2K7 | 89% 52% 36% | 101 5 854 | 1723 208 961 |
| HSQFH29 | 967708 | 534 | HMMER 1.8 | PFAM: ATPases associated with various cellular activities (AAA) | PF00004 | 97.36 | 193 | 393 |
| HTLEA35 | 1107230 | 162 | blastx.14 | (AF049099) SPAF [Mus musculus] | gi 4105619 gb AAD0 2481.1 | 83% 43% 76% 61% | 70 76 408 3 | 417 414 470 41 |
| HTLEA35 | 827028 | 535 | HMMER 1.8 | (AK001571) unnamed protein product [Homo sapiens] | gi 7022907 dbj BAA9 1764.1 | 100% | 3 | 479 |
| HUVGG63 | 969432 | 536 | HMMER 1.8 | PFAM: ATPases associated with various cellular activities (AAA) | PF00004 | 332.15 | 621 | 1178 |
| HAGAX57 | 1150865 | 164 | blastx.14 | (AF159063) SKD1- homolog [Homo sapiens] | gi 5732691 gb AAD4 9227.1 AF159063_1 | 97% | 138 | 1448 |
| HAGAX57 | 1150865 | 164 | blastx.14 | (AF176012) J domain | gi 5815353 gb AAD5 | 100% | 192 | 785 |

| | | | | | | | | |
|---------|---------|-----|-----------------------------|--|---|--|--|--|
| HAGAX57 | 949211 | 537 | HMMER 1.8 blastx.14 | containing protein 1 isoform a [Homo sapiens] PFAM: DnaJ, prokaryotic heat shock protein (AF176012) J domain containing protein 1 isoform a [Homo sapiens] | 2650.1 AF176012_1 PF00226 gi 5815353 gb AAD5 2650.1 AF176012_1 | 67.6 100% | 224 185 | 421 778 |
| HAMGX15 | 1177932 | 165 | blastx.14 | (AL032657) predicted using Genefinder; similar to 111 ES | gi 3881075 emb CAA 21734.1 | 64% 52% 66% 32% 45% 26% | 335 560 665 623 674 626 | 565 667 736 733 733 751 |
| HAMGX15 | 908840 | 538 | HMMER 2.1.1 blastx.14 | PFAM: DnaJ domain (AL032657) predicted using Genefinder; similar to 111 ES | PF00226 gi 3881075 emb CAA 21734.1 | 80.1 51% | 554 506 | 709 715 |
| HAUBV06 | 1106041 | 166 | blastx.14 | similar to [SwissProt Accession Number P08409]; 1 | gi 1799806 dbj BAA1 6264.1 | 98% 80% | 1164 2104 | 2120 2166 |
| HAUBV06 | 596802 | 539 | HMMER 2.1.1 | PFAM: DnaJ C terminal region | PF01556 | 262.1 | 567 | 932 |
| HAUBV06 | 929762 | 540 | HMMER 2.1.1 | PFAM: DnaJ C terminal region | PF01556 | 249.7 | 1650 | 1285 |
| HBWCM62 | 908818 | 541 | HMMER 1.8 blastx.14 | PFAM: DnaJ, prokaryotic heat shock protein contains strong similarity to a DNAJ-like domain (PS:PS00636) [Caenorhabditis elegans] | PF00226 gi 1707079 gb AAB3 7835.1 | 97.9 42% | 37 19 | 243 306 |

| | | | | | | | | |
|---------|---------|-----|-------------|---|-------------------------------------|--------|-----|-----|
| HCWFA35 | 1105672 | 168 | blastx.14 | Curved DNA-binding protein cbpA [Escherichia coli] | gi 1651491 dbj BAA36142.1 | 98% | 68 | 322 |
| HCWFA35 | 908820 | 542 | HMMER 1.8 | PFAM: DnaJ, prokaryotic heat shock protein | PF00226 | 116.61 | 80 | 274 |
| | | | blastx.14 | Curved DNA-binding protein cbpA [Escherichia coli] | gi 1651491 dbj BAA36142.1 | 98% | 68 | 364 |
| HDACA35 | 1107236 | 169 | blastx.14 | (AK001496) unnamed protein product [Homo sapiens] | gi 7022789 dbj BAA91724.1 | 76% | 71 | 904 |
| HDACA35 | 908837 | 543 | HMMER 1.8 | PFAM: DnaJ, prokaryotic heat shock protein | PF00226 | 65.68 | 68 | 229 |
| | | | blastx.14 | cysteine string protein [Bos taurus] | gi 1232165 emb CAA63355.1 | 49% | 80 | 256 |
| HDQGM08 | 1151469 | 170 | blastx.14 | (AF176013) J domain containing protein 1 isoform b [Homo sapiens] | gi 5815355 gb AAD52651.1 AF176013_1 | 100% | 37 | 357 |
| HDQGM08 | 949210 | 544 | HMMER 1.8 | PFAM: DnaJ, prokaryotic heat shock protein | PF00226 | 68.48 | 466 | 269 |
| | | | blastx.14 | (AF176013) J domain containing protein 1 isoform b [Homo sapiens] | gi 5815355 gb AAD52651.1 AF176013_1 | 100% | 505 | 185 |
| HELGB06 | 1148741 | 171 | blastx.14 | ORF-1 [Escherichia coli] | gi 402674 gb AAA18299.1 | 100% | 248 | 3 |
| HELGB06 | 935730 | 545 | HMMER 2.1.1 | PFAM: DnaJ domain | PF00226 | 78.3 | 203 | 421 |
| | | | blastx.14 | ORF-1 [Escherichia coli] | gi 402674 gb AAA18299.1 | 100% | 200 | 445 |
| HEOPR74 | 908836 | 546 | HMMER 1.8 | PFAM: DnaJ, prokaryotic heat shock protein | PF00226 | 88.67 | 65 | 262 |

| | | | | | | | | |
|---------|---------|-----|----------------|--|-------------------------------|-------|-----|------|
| HIBEK35 | 731480 | 173 | blastx.14 | cysteine string protein [Bos taurus] | gi 1232163 emb CAA 63354.1 | 41% | 68 | 289 |
| | | | HMMER 2.1.1 | PFAM: DnaJ domain | PF00226 | 50% | 457 | 492 |
| HJMAR88 | 908839 | 547 | HMMER 2.1.1 | PFAM: DnaJ domain | PF00226 | 112.7 | 237 | 404 |
| | | | blastx.14 | cysteine string protein 1 - human | pir S70515 S70515 | 68% | 6 | 254 |
| | | | HMMER 2.1.1 | PFAM: DnaJ domain | PF00226 | 100% | 1 | 60 |
| HMWGU56 | 908825 | 548 | HMMER 2.1.1 | PFAM: DnaJ domain | PF00226 | 126.9 | 375 | 569 |
| | | | blastx.14 | Similarity to B.subtilis DNAJ protein 1 [Caenorhabditis elegans] | gi 3873707 emb CAA 97416.1 | 59% | 327 | 587 |
| | | | | | | 65% | 630 | 698 |
| HOUDS09 | 1164010 | 176 | blastx.14 | (AK000034) unnamed protein product [Homo sapiens] | gi 7019854 dbj BAA9 0896.1 | 34% | 51 | 200 |
| | | | | | | 66% | 240 | 659 |
| | | | | | | 35% | 729 | 1118 |
| | | | | | | 45% | 96 | 167 |
| | | | | | | 32% | 174 | 248 |
| HOUDS09 | 949051 | 549 | HMMER 1.8 | PFAM: DnaJ, prokaryotic heat shock protein | PF00226 | 98.53 | 310 | 504 |
| | | | blastx.2 | (AK000034) unnamed protein product [Homo sapiens] | dbj BAA90896.1 | 53% | 37 | 888 |
| | | | | | | 55% | 899 | 1033 |
| | | | | | | 63% | 2 | 34 |
| HTEGM38 | 675087 | 177 | HMMER 2.1.1 | PFAM: DnaJ domain | PF00226 | 65.2 | 93 | 197 |
| HTEKY82 | 908846 | 550 | HMMER 2.1.1 | PFAM: DnaJ domain | PF00226 | 119.6 | 281 | 475 |
| | | | blastx.14 | Similarity to B.subtilis DNAJ protein 1 [Caenorhabditis elegans] | gi 3873707 emb CAA 97416.1 | 53% | 236 | 502 |
| | | | | | | | | |
| HTLCY54 | 1193550 | 179 | blastx.14 | MDJ6. | sp Q9QYI7 Q9QYI7 | 94% | 239 | 460 |
| | | | | | | 81% | 796 | 927 |

| | | | | | | | | |
|---------|--------|-----|-----------------------------|---|-------------------------------------|--------------------------|--------------------------|--------------------------|
| HTLCY54 | 908832 | 551 | HMMER 2.1.1 blastx.14 | PFAM: DnaJ domain (AB014888) MRJ [Homo sapiens] | PF00226 | 81% 73% 119.8 | 484 610 245 | 597 699 445 |
| HFOXK14 | 603245 | 180 | HMMER 1.8 | PFAM: Adenylate and Guanylate cyclase catalytic domain | PF00211 | 67% 78% 47% 40% | 239 797 632 611 | 616 934 694 691 |
| HHFFO69 | 837703 | 181 | HMMER 1.8 | PFAM: Adenylate and Guanylate cyclase catalytic domain | PF00211 | 137.85 | 183 | 401 |
| HHFLU06 | 857884 | 182 | HMMER 2.1.1 | PFAM: Adenylate and Guanylate cyclase catalytic domain | PF00211 | 386.54 | 124 | 708 |
| HAGBA56 | 732597 | 183 | HMMER 2.1.1 | PFAM: Eukaryotic protein kinase domain | PF00069 | 108.8 | 17 | 268 |
| HAGGF84 | 911312 | 184 | HMMER 1.8 blastx.14 | PFAM: Eukaryotic protein kinase domain calmodulin-dependent protein kinase II-delta dash [Oryctolagus cuniculus] | PF00069 | 64.9 | 139 | 516 |
| HAHGD33 | 921782 | 185 | HMMER 1.8 blastx.14 | PFAM: Eukaryotic protein kinase domain (AF145690) BeDNA.LD28657 [Drosophila melanogaster] | PF00069 | 105.85 | 10 | 318 |
| | | | | | gi 3241849 dbj BAA28870.1 | 88% 87% 100% | 10 366 320 | 363 413 364 |
| | | | | | gi 5052670 gb AAD38665.1 AF145690_1 | 83.68 | 4 | 564 |
| | | | | | | 68% 56% 60% 39% | 1 412 304 676 | 297 609 426 804 |

| | | | | | | | | |
|---------|--------|-----|----------------|--|--------------------|-------|-----|------------------|
| HAHIY08 | 962113 | 186 | HMMER 1.8 | PFAM: Eukaryotic protein kinase domain | PF00069 | 74.92 | 39 | 278 |
| | | | blastx.14 | similar to tyrosine kinase [Caenorhabditis elegans] | | | | |
| | | | | | | | | 278 92 179 |
| HBIOZ10 | 973131 | 187 | HMMER 1.8 | PFAM: Eukaryotic protein kinase domain | PF00069 | 121.1 | 3 | 365 |
| | | | blastx.2 | (AF003134) strong similarity to the CDC2/CDX subfamily of ser/thr protein kinases [Caenorhabditis elegans] | | | | |
| HBKDI30 | 729048 | 188 | HMMER 1.8 | PFAM: Eukaryotic protein kinase domain | PF00069 | 42.23 | 1 | 213 |
| | | | | | | | | |
| HBXBW40 | 706115 | 189 | HMMER 1.8 | PFAM: Eukaryotic protein kinase domain | PF00069 | 34.01 | 280 | 423 |
| | | | | | | | | |
| HCEHE35 | 909937 | 190 | HMMER 1.8 | PFAM: Eukaryotic protein kinase domain | PF00069 | 30.78 | 210 | 347 |
| | | | blastx.14 | protein kinase PRK2 [human, DX3 B-cell myeloma cell line, Peptide, 984 aa] [Homo sapiens] | | | | |
| HCEPW85 | 911374 | 191 | HMMER 1.8 | PFAM: Eukaryotic protein kinase domain | PF00069 | 83.52 | 3 | 260 |
| | | | blastx.14 | predicted using Genefinder; Similarity to 1111 cDNA | | | | |
| HCFAT25 | 932068 | 192 | HMMER 2.1.1 | PFAM: Eukaryotic protein kinase domain | PF00069 | 26.6 | 136 | 231 |
| | | | blastx.14 | (AF096300) HPK/GCK- | | | | |
| | | | | | gi 4322936 gb AAD1 | 63% | 91 | 456 |

| | | | | | | | | |
|---------|---------|-----|--------------------------|---|--|--------------|------------|-------------|
| HCFCF47 | 1139731 | 193 | blastx.14 | like kinase HGK [Homo sapiens] (AF003134) strong similarity to the CDC2/CDX 1 | 6137.1] | 72% 25% | 60 232 | 158 312 |
| HCFCF47 | 894415 | 552 | HMMER 1.8 | PFAM: Eukaryotic protein kinase domain | PF000069 | 89.54 | 20 | 295 |
| HDAAV61 | 810305 | 194 | HMMER 1.8 | PFAM: Eukaryotic protein kinase domain | PF000069 | 41.11 | 11 | 145 |
| HDPKD75 | 810824 | 195 | HMMER 1.8 | PFAM: Eukaryotic protein kinase domain | PF000069 | 98.74 | 68 | 433 |
| HDPNC96 | 934520 | 196 | HMMER 1.8 | PFAM: Eukaryotic protein kinase domain | PF000069 | 206.63 | 3 | 734 |
| HDPSR15 | 969666 | 197 | blastx.14 HMMER 1.8 | HUMAN NDR [unidentified] PFAM: Eukaryotic protein kinase domain | gi 2304746 emb CAA03387.1 PF000069 | 92% 87.19 | 3 351 | 734 626 |
| HDQDX20 | 919027 | 198 | blastx.2 HMMER 2.1.1 | (AB026289) protein kinase SID6-1512 [Homo sapiens] PFAM: PX domain | dbj BAA85045.1 PF00787 | 95% 73.4 | 631 246 | 1158 569 |
| HDQHB19 | 895106 | 553 | blastx.14 HMMER 2.1.1 | serine/threonine protein kinase [Rattus norvegicus] PFAM: Eukaryotic protein kinase domain | gi 294637 gb AAA42137.1 PF000069 | 78% 92.5 | 633 260 | 974 520 |
| HDTBY88 | 934472 | 200 | HMMER 2.1.1 | PFAM: Eukaryotic protein kinase domain | PF000069 | 93.6 | 3 | 302 |
| | | | blastx.14 | p56 KKIAMRE protein kinase [Homo sapiens] | gi 1517820 gb AAC50918.1 | 82% 35% | 3 192 | 170 458 |

| | | | | | | | | |
|---------|--------|-----|----------------------------|---|-------------------------------|---------------------|-----------------|-------------------|
| HE2KZ07 | 909948 | 201 | HMMER 1.8 blastx.14 | PFAM: Eukaryotic protein kinase domain (AB004267) Ca2+/calmodulin- dependent protein kinase I beta 2 [Rattus norvegicus] | gi 3135197 dbj BAA2 8263.1 | 100% 115.19 | 492 5 | 509 289 |
| HE8UY74 | 960914 | 202 | HMMER 1.8 blastx.14 | PFAM: Eukaryotic protein kinase domain (AF080119) contains similarity to protein kinase 1 | gi 3600036 gb AAC3 5524.1 | 96% 56% 36.37 | 17 418 | 433 507 |
| HE9NO66 | 974353 | 203 | HMMER 1.8 blastx.14 | PFAM: Eukaryotic protein kinase domain (AB020741) NIK-related kinase [Mus musculus] | gi 6009519 dbj BAA8 4943.1 | 73% 94% 79% | 449 2 748 | 817 283 990 |
| HEMBT61 | 939957 | 204 | HMMER 2.1.1 blastx.2 | PFAM: Eukaryotic protein kinase domain (AD000092) hypothetical human serine-threonine protein kinase R31240_1 [Homo sapiens] | gb AAB51171.1 | 76.6% 71% | 16 13 | 285 441 |
| HETLF29 | 909762 | 205 | HMMER 1.8 blastx.14 | PFAM: Eukaryotic protein kinase domain similar to cAMP- dependant protein kinase; cDNA EST 111 | gi 3878636 emb CAA 88953.1 | 143.18 56% | 6 6 | 416 416 |
| HFIUE75 | 909758 | 206 | HMMER 1.8 | PFAM: Eukaryotic protein kinase domain | PF000069 | 85.68 | 377 | 664 |

| | | | | | | | | |
|---------|--------|-----|-------------|---|-------------------------------------|------------|------------|------------|
| | | | blastx.14 | (AD000092) hypothetical human serine-threonine protein kinase R31240_1 [Homo sapiens] | gi 1905906 gb AAB51171.1 | 43% | 362 | 634 |
| HFKIT06 | 934019 | 207 | HMMER 1.8 | PFAM: Eukaryotic protein kinase domain | PF00069 | 34.65 | 160 | 270 |
| | | | blastx.14 | p58 galactosyltransferase-associated protein kinase - human | pir A38282 A38282 | 51% 40% | 178 74 | 270 118 |
| HHEGG20 | 894409 | 208 | HMMER 1.8 | PFAM: Eukaryotic protein kinase domain | PF00069 | 200.01 | 26 | 598 |
| HHEHC53 | 921783 | 209 | HMMER 1.8 | PFAM: Eukaryotic protein kinase domain | PF00069 | 58.81 | 507 | 797 |
| | | | blastx.14 | (AF145690) BcDNA.LD28657 [Drosophila melanogaster] | gi 5052670 gb AAD38665.1 AF145690_1 | 79% 70% | 567 321 | 803 563 |
| HHERQ79 | 944057 | 210 | HMMER 1.8 | PFAM: Eukaryotic protein kinase domain | PF00069 | 83.4 | 133 | 474 |
| | | | blastx.2 | (AB016589) inducible IKappaB kinase [Mus musculus] | dbj BAA85154.1 | 90% | 109 | 471 |
| HISAF59 | 959140 | 211 | HMMER 1.8 | PFAM: Eukaryotic protein kinase domain | PF00069 | 89.46 | 340 | 771 |
| | | | blastx.14 | (AC002343) Ser/Thr protein kinase isolog [Arabidopsis thaliana] | gi 2262107 gb AAB63615.1 | 39% 33% | 460 397 | 768 468 |
| HKAKM10 | 918685 | 212 | HMMER 2.1.1 | PFAM: Eukaryotic protein kinase domain | PF00069 | 31.4 | 8 | 127 |
| HLTHP86 | 919354 | 213 | HMMER 2.1.1 | PFAM: TBC domain | PF00566 | 69.4 | 855 | 1274 |
| | | | blastx.2 | (AF161420) HSPC302 | gb AAF28980.1 AF1 | 89% | 456 | 1352 |

| | | | | | | | | |
|---------|--------|-----|--------------|---|---|--|---|--|
| HMSJL96 | 934483 | 214 | HMMER 1.8 | [Homo sapiens] PFAM: Eukaryotic protein kinase domain | 61420_1 | 99% 52% | 1309 1253 | 1974 1309 |
| HMTAJ73 | 813296 | 215 | HMMER 1.8 | PFAM: Eukaryotic protein kinase domain | PF000069 | 26.49 | 199 | 363 |
| HNTCP13 | 909770 | 216 | HMMER 1.8 | PFAM: Eukaryotic protein kinase domain | PF000069 | 21.34 | 4 | 114 |
| | | | blastx.14 | PFAM: Eukaryotic protein kinase domain | PF000069 | 102.96 | 445 | 930 |
| | | | blastx.14 | (AC006530) unknown [Homo sapiens] | gi 4809337 gb AAD3 0182.1 AC006530_4 | 55% | 463 | 957 |
| HNTMD79 | 934522 | 217 | HMMER 1.8 | PFAM: Eukaryotic protein kinase domain | PF000069 | 130.82 | 203 | 586 |
| | | | blastx.14 | LATS [Drosophila melanogaster] | gi 903942 gb AAA70 336.1 | 52% 33% 57% 22% | 239 76 169 64 | 586 156 210 240 |
| HNTMH70 | 757184 | 218 | HMMER 1.8 | PFAM: Eukaryotic protein kinase domain | PF000069 | 94.55 | 176 | 577 |
| HNTNB14 | 909942 | 219 | HMMER 1.8 | PFAM: Eukaryotic protein kinase domain | PF000069 | 96.28 | 38 | 343 |
| | | | blastx.14 | calmodulin-binding protein [Rattus norvegicus] | gi 349075 gb AAA16 633.1 | 97% 85% 74% 77% 69% 65% 60% 52% 37% 39% 35% 33% | 41 553 553 553 559 553 553 553 553 553 553 559 | 475 657 657 657 657 657 657 654 657 636 645 657 |

| | | | | | | | | |
|---------|--------|-----|----------------------------|--|------------------------------|----------------------------------|--------------------------------|---------------------------------|
| HODFF88 | 974911 | 220 | HMMER 1.8 blastx.14 | PFAM: Eukaryotic protein kinase domain mixed-lineage protein kinase 1 - human | PF00069 pir S32467 JU0229 | 77% 29% 101.43 | 512 556 98 | 538 657 370 |
| HOHCE47 | 911566 | 554 | HMMER 1.8 | PFAM: Eukaryotic protein kinase domain | PF00069 | 79.42 | 211 | 423 |
| HPCRV84 | 945856 | 222 | HMMER 1.8 blastx.2 | PFAM: Eukaryotic protein kinase domain similar to protein kinase of X.laevis, has putative 1 | PF00069 dbj BAA11492.1 | 75.57 78% | 157 127 | 384 483 |
| HRACK83 | 888037 | 223 | HMMER 1.8 | PFAM: Eukaryotic protein kinase domain | PF00069 | 48.4 | 211 | 423 |
| HRADM45 | 717358 | 224 | HMMER 1.8 blastx.2 | PFAM: Eukaryotic protein kinase domain (AJ271722) putative serine/threonine protein kinase MAK-V [Homo sapiens] | PF00069 emb CAB71146.1 | 23.7 98% | 14 2 | 124 469 |
| HRAED74 | 942527 | 225 | HMMER 1.8 blastx.2 | PFAM: Eukaryotic protein kinase domain (AB023658) Ca/calmodulin-dependent protein kinase kinase alpha, CaM-kinase kinase alpha [Rattus norvegicus] | PF00069 dbj BAA75246.1 | 59.6 97% 81% 71% 88% | 406 71 388 342 662 | 612 346 648 425 688 |
| HRDZ70 | 942673 | 226 | HMMER 2.1.1 blastx.2 | PFAM: Eukaryotic protein kinase domain kinase like protein | PF00069 emb CAB10257.1 | 78.2 39% | 33 33 | 248 323 |

| | | | | | | | | |
|---------|---------|-----|----------------|---|-------------------------------|--------------------------|-------------------------|---------------------------|
| HSKAC24 | 823869 | 227 | HMMER 1.8 | [Arabidopsis thaliana] PFAM: Eukaryotic protein kinase domain | PF000069 | 50% | 303 | 380 |
| HSSMT34 | 911294 | 228 | HMMER 1.8 | PFAM: Eukaryotic protein kinase domain | PF000069 | 53.16 | 95 | 292 |
| HT3BG12 | 921593 | 229 | HMMER 1.8 | PFAM: Eukaryotic protein kinase domain | PF000069 | 27.09 | 109 | 183 |
| | | | blastx.14 | CYCLIN-DEPENDENT KINASE (CDK)8 [unidentified] | gi 3715669 emb CAA 03585.1 | 85% | 1 | 246 |
| HTEGO05 | 932583 | 230 | HMMER 2.1.1 | PFAM: Eukaryotic protein kinase domain | PF000069 | 50.8 | 3 | 233 |
| | | | blastx.14 | male germ cell-associated kinase (mak) [Rattus norvegicus] | gi 2052278 gb AAA41 562.1 | 85% 64% 85% 38% | 3 489 768 1023 | 395 761 848 1100 |
| HTEKT33 | 953308 | 231 | HMMER 1.8 | PFAM: Eukaryotic protein kinase domain | PF000069 | 200.58 | 428 | 1393 |
| | | | blastx.2 | (AC007661) putative protein kinase [Arabidopsis thaliana] | gb AAD32787.1 AC0 07661_24 | 41% 36% 29% | 722 1070 428 | 1009 1243 628 |
| HTEMU66 | 944419 | 232 | HMMER 1.8 | PFAM: Eukaryotic protein kinase domain | PF000069 | 114.85 | 613 | 963 |
| | | | blastx.2 | MEK Kinase 3 [Mus musculus] | gb AAB03535.1 | 49% 29% | 604 209 | 948 340 |
| HTEMV09 | 909843 | 233 | HMMER 1.8 | PFAM: Eukaryotic protein kinase domain | PF000069 | 99.16 | 19 | 312 |
| | | | blastx.14 | protein kinase I [Rattus norvegicus] | gi 406113 gb AAA19 670.1 | 44% | 1 | 321 |
| HTEMV66 | 1151075 | 234 | blastx.14 | contains EGF-like repeats; highly similar to ZC84.1; | gi 495684 gb AAA50 735.1 | 55% 44% | 579 783 | 223 649 |

| | | | | | | | | | |
|---------|---------|-----|----------------|---|---|--|--------|------|------|
| | | | | 1 | | | | | |
| HTEMV66 | 813038 | 555 | HMMER 2.1.1 | PFAM: Eukaryotic protein kinase domain | PF00069 | | 23% | 861 | 772 |
| HTGAU79 | 1175071 | 235 | blastx.14 | (AL157917) similarity to endopeptidases 1 | gi 7106102 emb CAB 76028.1 | | 27.8 | 154 | 315 |
| HTGAU79 | 940369 | 556 | HMMER 1.8 | PFAM: Eukaryotic protein kinase domain | PF00069 | | 50% | 755 | 976 |
| HTLEJ11 | 973302 | 236 | blastx.2 | (AL157917) similarity to endopeptidases [Schizosaccharomyces 1 | emb CAB76028.1 | | 38% | 371 | 571 |
| HTLIY52 | 1218691 | 237 | HMMER 2.1.1 | PFAM: Eukaryotic protein kinase domain | PF00069 | | 60% | 641 | 730 |
| HTLIY52 | 942161 | 557 | blastx.14 | (AF144573) Mx- interacting protein kinase PKM [Mesocricetus auratus] | gi 4868443 gb AAD3 1319.1 AF144573_1 | | 52% | 323 | 373 |
| HTOAK34 | 966800 | 238 | HMMER 1.8 | TESTIS-SPECIFIC SERINE/THREONINE KINASE. | sp Q61241 Q61241 | | 31.25 | 315 | 779 |
| | | | blastx.2 | PFAM: Eukaryotic protein kinase domain | PF00069 | | 45% | 324 | 977 |
| | | | HMMER 1.8 | PFAM: Eukaryotic protein kinase domain | PF00069 | | 55.9 | 44 | 223 |
| | | | blastx.14 | (AF144573) Mx- interacting protein kinase PKM [Mesocricetus auratus] | gi 4868443 gb AAD3 1319.1 AF144573_1 | | 69% | 35 | 268 |
| | | | HMMER 1.8 | PFAM: Eukaryotic protein kinase domain | PF00069 | | 40% | 437 | 592 |
| | | | blastx.2 | PFAM: Eukaryotic protein kinase domain | PF00069 | | 42% | 293 | 397 |
| | | | HMMER 1.8 | PFAM: Eukaryotic protein kinase domain | PF00069 | | 38% | 877 | 939 |
| | | | blastx.14 | PFAM: Eukaryotic protein kinase domain | PF00069 | | 46% | 640 | 972 |
| | | | HMMER 1.8 | PFAM: Eukaryotic protein kinase domain | PF00069 | | 48% | 142 | 414 |
| | | | blastx.2 | PFAM: Eukaryotic protein kinase domain | PF00069 | | 45% | 427 | 579 |
| | | | HMMER 1.8 | PFAM: Eukaryotic protein kinase domain | PF00069 | | 42% | 565 | 621 |
| | | | blastx.14 | PFAM: Eukaryotic protein kinase domain | PF00069 | | 251.19 | 166 | 933 |
| | | | HMMER 1.8 | PFAM: Eukaryotic protein kinase domain | PF00069 | | 44% | 133 | 936 |
| | | | blastx.2 | PFAM: Eukaryotic protein kinase domain | PF00069 | | 32.41 | 1020 | 1190 |
| | | | HMMER 1.8 | PFAM: Eukaryotic protein kinase domain | PF00069 | | 75% | 954 | 1190 |
| | | | blastx.14 | (AF084205) serine/threonine protein kinase TAO1 [Rattus | gi 3452473 gb AAC7 1014.1 | | | | |

| | | | | | | | | |
|---------|---------|-----|---------------------------|---|--|---|--|--|
| HTPGG25 | 911282 | 239 | HMMER 1.8 blastx.2 | norvegicus] PFAM: Eukaryotic protein kinase domain (AL117482) hypothetical protein [Homo sapiens] | PF000069 emb CAB55955.1 | 114.02 | 72 | 353 |
| HUJAD24 | 1161319 | 240 | blastx.14 | serine/threonine kinase [Rattus norvegicus] | gi 2052191 emb CAB 06295.1 | 34% 48% 34% 57% 48% 24% 47% 72% 42% | 439 345 779 267 123 57 3 211 162 | 759 494 910 344 215 206 53 243 218 |
| HUJAD24 | 911498 | 558 | HMMER 1.8 blastx.14 | PFAM: Eukaryotic protein kinase domain AMP-activated protein kinase homolog [Homo sapiens] | PF000069 gi 758783 gb AA64 850.1 | 34.73 | 9 | 215 |
| HUTSF11 | 966029 | 241 | HMMER 1.8 blastx.14 | PFAM: Eukaryotic protein kinase domain PRO1038. | PF000069 | 27.74 | 3 | 104 |
| HUVGZ88 | 1227628 | 242 | blastx.14 | | sp AAAF71042 AAAF71 042 | 59% 41% 39% 75% | 425 1159 1282 1695 | 859 1296 1404 1742 |
| HUVGZ88 | 959020 | 559 | HMMER 1.8 blastx.14 | PFAM: Eukaryotic protein kinase domain (AF191838) TANK binding kinase TBK1 | PF000069 | 31.12 | 182 | 439 |
| HWADY66 | 1096252 | 243 | blastx.14 | | gi 6224868 gb AAAF05 989.1 AF191838.1 | 84% | 10 | 183 |

| | | | | | | | | |
|---------|---------|-----|----------------------------|--|--|-----------------------------------|--------------------------------------|------------------------------------|
| HWADY66 | 734565 | 560 | HMMER 1.8 | [Homo sapiens] PFAM: Eukaryotic protein kinase domain | PF00069 | 28.82 | 1 | 174 |
| HWAFG04 | 952878 | 244 | HMMER 1.8 blastx.14 | PFAM: Eukaryotic protein kinase domain (AC002343) Ser/Thr protein kinase isolog [Arabidopsis thaliana] | PF00069 gi 2262107 gb AAB6 3615.1 | 93.74 41% 48% 42% 75% | 1655 1655 1319 1046 1355 | 945 1383 1185 933 1332 |
| HWAFS18 | 948434 | 245 | HMMER 1.8 blastx.14 | PFAM: Eukaryotic protein kinase domain (AF156884) RIP-like kinase [Homo sapiens] | PF00069 gi 5059425 gb AAD3 9005.1 AF156884_1 | 115.98 91% 66% 100% | 225 165 702 632 | 632 632 773 661 |
| HWAGS73 | 1150212 | 246 | blastx.14 | (AF156884) RIP-like kinase [Homo sapiens] | gi 5059425 gb AAD3 9005.1 AF156884_1 | 82% | 1 | 273 |
| HWAGS73 | 894404 | 561 | HMMER 1.8 | PFAM: Eukaryotic protein kinase domain | PF00069 | 64.17 | 4 | 273 |
| HWLEA48 | 927676 | 247 | HMMER 1.8 blastx.2 | PFAM: Eukaryotic protein kinase domain (AF169034) protein kinase [Homo sapiens] | PF00069 gb AAF12757.2 AF1 69034_1 | 32.82 59% 100% 51% | 190 154 89 287 | 381 429 166 415 |
| HWLHS82 | 934505 | 248 | HMMER 2.1.1 blastx.2 | PFAM: Eukaryotic protein kinase domain (AC005581) R31237_1, partial CDS [Homo sapiens] | PF00069 gb AAC33487.1 | 147.2 90% 100% 40% | 2 68 2 306 | 319 364 76 422 |
| HWMTB81 | 955336 | 249 | HMMER 1.8 blastx.2 | PFAM: Eukaryotic protein kinase domain (AK000528) unnamed | PF00069 dbj BAA91232.1 | 122.85 100% | 1458 3 | 934 572 |

| | | | | | | | | |
|---------|---------|-----|-------------|---|-------------------------------------|-------------------|---------------------|---------------------|
| HCWDV17 | 1105673 | 250 | blastx.14 | protein product [Homo sapiens] BvgA positive transcription regulator (put.); putative [Bordetella pertussis] | gi 144039 gb AAA22969.1 | 57% 70% | 203 77 | 604 187 |
| HCWDV17 | 974478 | 562 | HMMER 1.8 | PFAM: Bacterial regulatory proteins, luxR family | PF00196 | 81.59 | 416 | 613 |
| HELDI95 | 1103374 | 251 | blastx.14 | Regulatory protein KdpD. [Escherichia coli] | gi 1651302 dbj BAA35352.1 | 100% | 103 | 525 |
| HELDI95 | 953059 | 563 | HMMER 1.8 | PFAM: Response regulator receiver domain | PF00072 | 123.84 | 482 | 766 |
| HAGFO25 | 1150845 | 252 | blastx.14 | Regulatory protein KdpD. [Escherichia coli] | gi 1651302 dbj BAA35352.1 | 98% | 1 | 432 |
| HAGFO25 | 957992 | 564 | HMMER 1.8 | (AF062595) adenylate kinase 5 [Homo sapiens] | gi 4691541 gb AAD27956.1 AF062595_1 | 92% | 145 | 732 |
| HAWAB54 | 1149319 | 253 | blastx.14 | PFAM: Adenylate kinases | PF00406 | 206.82 | 180 | 650 |
| HAWAB54 | 957993 | 565 | HMMER 2.1.1 | (AF062595) adenylate kinase 5 [Homo sapiens] | gi 4691541 gb AAD27956.1 AF062595_1 | 90% | 135 | 728 |
| HLIBV06 | 934887 | 254 | HMMER 2.1.1 | (AF062595) adenylate kinase 5 [Homo sapiens] | gi 4691541 gb AAD27956.1 AF062595_1 | 92% 30% 29% | 876 1341 1413 | 283 1012 1321 |
| | | | | PFAM: Adenylate kinase | PF00406 | 40.1 | 111 | 296 |
| | | | | (AF062595) adenylate kinase 5 [Homo sapiens] | gi 4691541 gb AAD27956.1 AF062595_1 | 98% | 111 | 374 |
| | | | | PFAM: Adenylate kinase | PF00406 | 100.8 | 81 | 245 |
| | | | blastx.14 | (AB020203) adenylate | gi 4760600 dbj BAA7 | 90% | 81 | 350 |

| | | | | | | | | |
|---------|---------|-----|-------------|--|--------------------------|--------------------------|--------------------------|---------------------------|
| HMALL66 | 1105097 | 255 | blastx.14 | kinase isozyme 3 [Mus musculus] | 7360.1 | | | |
| | | | | adenylate kinase (EC 2.7.4.3), chloroplast - maize | pir S45634 S45634 | 45% | 71 | 292 |
| HMALL66 | 956195 | 566 | HMMER 1.8 | PFAM: Adenylate kinases | PF00406 | 50.17 | 63 | 296 |
| HOACE12 | 858976 | 256 | HMMER 2.1.1 | PFAM: Adenylate kinase | PF00406 | 46.1 | 20 | 235 |
| HOGCG69 | 924848 | 257 | HMMER 1.8 | PFAM: Adenylate kinases | PF00406 | 76.14 | 858 | 1145 |
| | | | blastx.14 | adenylate kinase (EC 2.7.4.3), chloroplast - maize | pir S45634 S45634 | 36% 35% 33% 57% | 480 849 379 214 | 791 1145 522 255 |
| HAGAE09 | 525926 | 567 | HMMER 1.8 | PFAM: Phorbol esters / diacylglycerol binding domain | PF00130 | 3.93 | 159 | 185 |
| HAGAE34 | 525878 | 568 | HMMER 1.8 | PFAM: Phorbol esters / diacylglycerol binding domain | PF00130 | 8.88 | 191 | 253 |
| HARMH78 | 1137572 | 260 | blastx.14 | (AF001435) unknown [Homo sapiens] | gi 2529709 gb AAB81205.1 | 32% 43% 75% | 237 135 482 | 395 203 505 |
| HARMH78 | 773210 | 569 | HMMER 1.8 | PFAM: Phorbol esters / diacylglycerol binding domain | PF00130 | 4.88 | 192 | 227 |
| HBILB53 | 974122 | 570 | HMMER 1.8 | PFAM: Phorbol esters / diacylglycerol binding domain | PF00130 | 4.62 | 301 | 348 |
| HBJNB52 | 726475 | 571 | HMMER | PFAM: Phorbol esters / | PF00130 | 3.77 | 193 | 252 |

| | | | | | | | | |
|---------|---------|-----|-----------|--|---------------------------|-------------------|---------------------|---------------------|
| HDABQ83 | 669619 | 572 | 1.8 | diacylglycerol binding domain | PF00130 | 6.04 | 255 | 284 |
| HDPDC84 | 616980 | 573 | HMMER 1.8 | PFAM: Phorbol esters / diacylglycerol binding domain | PF00130 | 25.6 | 253 | 393 |
| HDPUF40 | 1212494 | 265 | blastx.14 | PTPL1-ASSOCIATED RHOGAP. | sp O15463 O15463 | 54% 46% 23% | 286 1018 1537 | 867 1230 1662 |
| HDPUF40 | 970586 | 574 | HMMER 1.8 | PFAM: Phorbol esters / diacylglycerol binding domain | PF00130 | 26.42 | 415 | 546 |
| | | | blastx.14 | similar to C.elegans protein (Z37093) [Homo sapiens] | gi 1504026 dbj BAA13212.1 | 94% 98% | 61 654 | 651 806 |
| HDPWU07 | 952734 | 575 | HMMER 1.8 | PFAM: Phorbol esters / diacylglycerol binding domain | PF00130 | 2.94 | 333 | 356 |
| HDTJJ02 | 913787 | 576 | HMMER 1.8 | PFAM: Phorbol esters / diacylglycerol binding domain | PF00130 | 5.7 | 21 | 68 |
| HE2GA18 | 1121872 | 268 | blastx.14 | mhpR [Escherichia coli] | gi 1702880 emb CAA70746.1 | 98% | 288 | 1 |
| HE2GA18 | 867276 | 577 | HMMER 1.8 | PFAM: Phorbol esters / diacylglycerol binding domain | PF00130 | 4.09 | 74 | 109 |
| HE2SY03 | 947947 | 578 | HMMER 1.8 | PFAM: Phorbol esters / diacylglycerol binding domain | PF00130 | 2.97 | 387 | 437 |

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|---------|---------|-----|--------------|---|---|-------------------|-------------------|------------------|
| HELGY64 | 934511 | 579 | HMMER 1.8 | (AF118023) SH3 domain- binding protein SNP70 [Homo sapiens] PFAM: Phorbol esters / diacylglycerol binding domain | gi 4836401 gb AAD3 0425.1 AF118023_1 | 46% | 456 | 301 |
| HFIYW31 | 697730 | 580 | HMMER 1.8 | PFAM: Phorbol esters / diacylglycerol binding domain | PF00130 | 76.38 | 241 | 390 |
| HFVIP88 | 960741 | 581 | HMMER 1.8 | PFAM: Phorbol esters / diacylglycerol binding domain | PF00130 | 3.29 | 29 | 67 |
| HGBAS76 | 771320 | 582 | HMMER 1.8 | PFAM: Phorbol esters / diacylglycerol binding domain | PF00130 | 7.32 | 147 | 206 |
| HHEBB62 | 1151481 | 274 | blastx.14 | PFAM: Phorbol esters / diacylglycerol binding domain | PF00130 | 3.23 | 322 | 348 |
| HHEBB62 | 791469 | 583 | HMMER 1.8 | (AK000193) unnamed protein product [Homo sapiens] PFAM: Phorbol esters / diacylglycerol binding domain | gi 7020117 dbj BAA9 1000.1 | 100% | 1 | 375 |
| HHEHU73 | 923895 | 584 | HMMER 1.8 | PFAM: Phorbol esters / diacylglycerol binding domain | PF00130 | 6.2 | 292 | 236 |
| HHEMA11 | 966924 | 585 | HMMER 1.8 | PFAM: Phorbol esters / diacylglycerol binding domain | PF00130 | 4.1 | 115 | 156 |
| HHEQK01 | 1107392 | 277 | blastx.14 | PFAM: Phorbol esters / diacylglycerol binding domain | PF00130 | 10.16 | 354 | 395 |
| HHEQK01 | 871911 | 586 | HMMER 1.8 | ORF 3 [Homo sapiens] PFAM: Phorbol esters / diacylglycerol binding domain | gi 182221 gb AAA58 464.1 | 37% 55% 39% | 165 266 342 | 22 213 274 |
| HHEQK01 | 871911 | 586 | HMMER 1.8 | PFAM: Phorbol esters / diacylglycerol binding domain | PF00130 | 3.27 | 64 | 90 |

| | | | | | | | | |
|---------|---------|-----|----------------|--|-------------------------------|--|---|--|
| HHPEM84 | 915639 | 278 | HMMER 1.8 | domain PFAM: Phorbol esters / diacylglycerol binding domain | PF00130 | 12.35 | 146 | 187 |
| HHSED84 | 706739 | 587 | HMMER 2.1.1 | PFAM: Sterol O- acyltransferase | PF01800 | 276.4 | 2 | 364 |
| HIBCC94 | 504326 | 588 | HMMER 1.8 | PFAM: Phorbol esters / diacylglycerol binding domain | PF00130 | 3.12 | 177 | 206 |
| HKADN56 | 1220254 | 281 | blastx.14 | CG5276 PROTEIN. | sp Q9VGN8 Q9VGN8 | 58% 68% 54% 43% 63% 47% 87% 42% | 904 1465 1279 796 754 706 1627 102 | 1257 1617 1437 891 810 756 1650 158 |
| HKADN56 | 968619 | 590 | HMMER 1.8 | PFAM: Phorbol esters / diacylglycerol binding domain | PF00130 | 5.32 | 207 | 233 |
| HKIXG58 | 464241 | 591 | HMMER 1.8 | PFAM: Phorbol esters / diacylglycerol binding domain | PF00130 | 3.59 | 84 | 137 |
| HLICI13 | 626559 | 592 | HMMER 1.8 | PFAM: Phorbol esters / diacylglycerol binding domain | PF00130 | 4.83 | 328 | 378 |
| HLTGF17 | 662405 | 284 | HMMER 1.8 | PFAM: Phorbol esters / diacylglycerol binding domain | PF00130 | 3.46 | 136 | 183 |
| HLYDC50 | 1151494 | 285 | blastx.14 | similar to C.elegans protein (Z37093) [Homo sapiens] | gi 1504026 dbj BAAI 3212.1 | 59% 52% 37% | 275 719 32 | 652 871 127 |

| | | | | | | | | |
|----------|---------|-----|--------------|---|-------------------|-------|------|-----|
| HL YDC50 | 677050 | 593 | HMMER 1.8 | PFAM: Phorbol esters / diacylglycerol binding domain | PF00130 | 29.67 | 191 | 319 |
| HMADD49 | 1217031 | 286 | blastx.14 | L-aspartate oxidase (EC 1.4.3.16) nadB [validated] -1 | pir E65035 OXECLD | 100% | 2212 | 803 |
| HMADD49 | 867481 | 594 | HMMER 1.8 | PFAM: Phorbol esters / diacylglycerol binding domain | PF00130 | 3.79 | 131 | 175 |
| HMEKE78 | 792383 | 595 | HMMER 1.8 | PFAM: Phorbol esters / diacylglycerol binding domain | PF00130 | 3.04 | 3 | 35 |
| HMSHU26 | 681745 | 596 | HMMER 1.8 | PFAM: Phorbol esters / diacylglycerol binding domain | PF00130 | 6.77 | 158 | 226 |
| HNEEB82 | 778884 | 597 | HMMER 1.8 | PFAM: Phorbol esters / diacylglycerol binding domain | PF00130 | 3.33 | 126 | 152 |
| HNHIA06 | 859932 | 598 | HMMER 1.8 | PFAM: Phorbol esters / diacylglycerol binding domain | PF00130 | 3.13 | 123 | 146 |
| HODFY16 | 958329 | 599 | HMMER 1.8 | PFAM: Phorbol esters / diacylglycerol binding domain | PF00130 | 3.15 | 175 | 213 |
| HPQSB68 | 740087 | 600 | HMMER 1.8 | PFAM: Phorbol esters / diacylglycerol binding domain | PF00130 | 3.9 | 170 | 247 |
| HRDBH04 | 922022 | 601 | HMMER 1.8 | PFAM: Phorbol esters / diacylglycerol binding domain | PF00130 | 5.19 | 600 | 632 |
| HSICR69 | 531061 | 602 | HMMER 1.8 | PFAM: Phorbol esters / diacylglycerol binding domain | PF00130 | 3.1 | 190 | 213 |

| | | | | | | | | |
|---------|---------|-----|----------------|---|------------------------------|----------------------------|--------------------------|----------------------------|
| HSIGJ94 | 793624 | 603 | HMMER 1.8 | domain | PF00130 | 3.15 | 207 | 239 |
| HSYBL15 | 1104299 | 296 | blastx.14 | (AF021935) mytonic dystrophy kinase-related Cdc42-binding kinase [Rattus norvegicus] | gi 2736151 gb AAC0 2941.1 | 94% | 2 | 931 |
| HSYBL15 | 660053 | 604 | HMMER 1.8 | PFAM: Phorbol esters / diacylglycerol binding domain | PF00130 | 22.31 | 2 | 70 |
| HTEKH29 | 855660 | 297 | HMMER 2.1.1 | PFAM: Phorbol esters/diacylglycerol binding domain (CI domain) | PF00130 | 42.4 | 1660 | 1803 |
| HTGEL46 | 685425 | 605 | HMMER 1.8 | PFAM: Phorbol esters / diacylglycerol binding domain | PF00130 | 7.26 | 398 | 433 |
| HTGFA05 | 972982 | 606 | HMMER 1.8 | PFAM: Phorbol esters / diacylglycerol binding domain | PF00130 | 4.17 | 905 | 855 |
| HTLDU61 | 530316 | 607 | blastx.2 | phosphorylation regulatory protein HP-10 - human | pir A61382 A61382 | 99% 100% 74% 100% | 214 1080 827 67 | 909 1259 1078 213 |
| | | | HMMER 1.8 | PFAM: Phorbol esters / diacylglycerol binding domain | PF00130 | 5.45 | 102 | 125 |
| HTOFT34 | 527144 | 608 | HMMER 1.8 | PFAM: Phorbol esters / diacylglycerol binding domain | PF00130 | 4.53 | 235 | 264 |
| HTTDH46 | 1152491 | 302 | blastx.14 | F10B5.8 [Caenorhabditis] | gi 5824432 emb CAB | 74% | 32 | 607 |

| | | | | | | | | |
|---------|---------|-----|----------------|--|-------------------------------|-------------|------------|------------|
| HTTDH46 | 951114 | 609 | HMMER 1.8 | elegans] PFAM: Phorbol esters / diacylglycerol binding domain | 54223.1 PF00130 | 70% | 623 | 1144 |
| | | | blastx.14 | F10B5.8 [Caenorhabditis elegans] | gi 5824432 emb CAB 54223.1 | 73% 73% | 117 2 | 437 124 |
| HTTIO05 | 931037 | 610 | HMMER 1.8 | PFAM: Phorbol esters / diacylglycerol binding domain | PF00130 | 4.25 | 1289 | 1330 |
| HWHGY45 | 911621 | 304 | HMMER 1.8 | PFAM: Phorbol esters / diacylglycerol binding domain | PF00130 | 10.67 | 123 | 203 |
| HWLQR48 | 914556 | 611 | HMMER 1.8 | PFAM: Phorbol esters / diacylglycerol binding domain | PF00130 | 4.03 | 359 | 391 |
| HWLQX76 | 894607 | 612 | HMMER 2.1.1 | PFAM: RhoGAP domain | PF00620 | 97.4 | 715 | 963 |
| HATDD09 | 1165331 | 307 | blastx.14 | (AK000239) unnamed protein product [Homo sapiens] | gi 7020190 dbj BAA9 1027.1 | 52% | 3 | 260 |
| HATDD09 | 573794 | 613 | HMMER 1.8 | PFAM: Cyclic nucleotide- binding domain | PF00027 | 9.43 | 59 | 124 |
| HBJGT03 | 923800 | 614 | HMMER 1.8 | PFAM: Cyclic nucleotide- binding domain | PF00027 | 8.96 | 41 | 100 |
| HMTMF45 | 1141737 | 309 | blastx.14 | (AL109657) dJ842G6.1 (novel protein) [Homo sapiens] | gi 6691957 emb CAB 65791.1 | 96% 100% | 108 476 | 377 700 |
| HMTMF45 | 553382 | 615 | HMMER 1.8 | PFAM: Cyclic nucleotide- binding domain | PF00027 | 8.27 | 230 | 292 |
| HHPDV86 | 522953 | 310 | HMMER 2.1.1 | PFAM: PH domain | PF00169 | 33 | 196 | 531 |

| | | | | | | | | |
|---------|--------|-----|----------------|--|---|--------------------|-------------------|--------------------|
| HE8BT56 | 732602 | 311 | HMMER 2.1.1 | PFAM: Ras family | PF00071 | 46.1 | 138 | 248 |
| HUJDH06 | 907613 | 312 | HMMER 2.1.1 | PFAM: ADP-ribosylation factor family | PF00025 | 62.3 | 433 | 669 |
| | | | blastx.14 | (AF143680) arf-like protein 2 [Mus musculus] | gi 4929218 gb AAD3 3908.1 AF143680.1 | 32% 48% | 421 264 | 663 356 |
| HOEJG61 | 907614 | 313 | HMMER 2.1.1 | PFAM: ADP-ribosylation factor family | PF00025 | 45.6 | 399 | 566 |
| | | | blastx.14 | (AF031903) ADP- ribosylation-like factor homolog ARL6 [Mus musculus] | gi 3687625 gb AAC6 2194.1 | 75% 48% | 399 566 | 566 652 |
| HE8PN24 | 907620 | 314 | HMMER 1.8 | PFAM: ADP-ribosylation factors (Arf family) (contains ATP/GTP binding P-loop) | PF00025 | 104.77 | 197 | 568 |
| | | | blastx.14 | ADP-ribosylation factor [Candida albicans] | gi 727191 gb AAA64 266.1 | 38% 34% | 191 386 | 430 568 |
| HGBHI37 | 909745 | 315 | HMMER 2.1.1 | PFAM: PH domain | PF00169 | 30.1 | 107 | 259 |
| | | | blastx.14 | (AF017368) faciogenital dysplasia protein 2 [Mus musculus] | gi 3599940 gb AAC3 5430.1 | 82% 63% | 14 145 | 151 201 |
| HCHOK82 | 909755 | 316 | HMMER 2.1.1 | PFAM: RhoGEF domain | PF00621 | 176.8 | 40 | 519 |
| | | | blastx.14 | (AF017369) faciogenital dysplasia protein 3 [Mus musculus] | gi 3599942 gb AAC3 5431.1 | 90% 79% 100% | 31 855 1062 | 849 941 1082 |
| HFPCH24 | 912608 | 317 | HMMER 1.8 | PFAM: Ras family (contains ATP/GTP binding P-loop) | PF00071 | 43.25 | 47 | 307 |

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|---------|--------|-----|-------------|---|---------------------------|-------|-----|-----|
| | | | blastx.14 | rap2b gene product (AA 1-183) [Homo sapiens] | gi 35863 emb CAA37178.1 | 41% | 35 | 229 |
| HTTKF86 | 912689 | 318 | HMMER 2.1.1 | PFAM: Ras family | PF00071 | 29.6 | 98 | 223 |
| HCESA79 | 912709 | 319 | HMMER 2.1.1 | PFAM: Ras family | PF00071 | 45.1 | 67 | 243 |
| | | | blastx.14 | (AB027137) RAB-26 [Homo sapiens] | gi 5931612 dbj BAA84707.1 | 92% | 52 | 246 |
| HDTBJ28 | 912714 | 320 | HMMER 2.1.1 | PFAM: Ras family | PF00071 | 28.1 | 21 | 137 |
| | | | blastx.14 | Rab12 protein [Canis familiaris] | gi 437985 emb CAA80471.1 | 88% | 21 | 98 |
| HDPBF48 | 912783 | 321 | HMMER 2.1.1 | PFAM: Ras family | PF00071 | 26.1 | 33 | 101 |
| | | | blastx.14 | (AL117204) predicted using Genefinder [Caenorhabditis elegans] | gi 5832782 emb CAB55120.1 | 48% | 123 | 209 |
| | | | | | | 55% | 258 | 338 |
| | | | | | | 68% | 33 | 89 |
| | | | | | | 53% | 429 | 467 |
| HTPFY55 | 912928 | 322 | HMMER 2.1.1 | PFAM: Ras family | PF00071 | 27.2 | 240 | 386 |
| | | | blastx.14 | similar to the RAS gene family [Caenorhabditis elegans] | gi 1572819 gb AAB09163.1 | 48% | 117 | 383 |
| | | | | | | 60% | 396 | 524 |
| HMSCM47 | 923632 | 323 | HMMER 2.1.1 | PFAM: ATPases associated with various cellular activities (AAA) | PF00004 | 121.1 | 65 | 652 |
| | | | blastx.2 | (AF033862) Lon protease [Arabidopsis thaliana] | gb AAC05085.1 | 65% | 5 | 673 |
| HEOQA56 | 925132 | 324 | HMMER | PFAM: Ras family | PF00071 | 62.8 | 53 | 154 |

| | | | 1.8 | (contains ATP/GTP binding P-loop) | | | | |
|---------|--------|-----|-------------|---|---------------------------|---------------------|--------------------|----------------------|
| | | | blastx.14 | GTP-binding protein [DiscoPyge ommata] | gi 213115 gb AAA49230.1 | 76% | 23 | 202 |
| HTPCQ24 | 925349 | 325 | HMMER 2.1.1 | PFAM: PH domain | PF00169 | 31 | 217 | 438 |
| HWAEI37 | 929481 | 326 | HMMER 2.1.1 | PFAM: MCM2/3/5 family | PF00493 | 59.7 | 8 | 415 |
| | | | blastx.14 | (AL035461) dJ967N21.5 (novel MCM2/3/5 family member) [Homo sapiens] | gi 5834569 emb CAB55276.1 | 100% 92% | 323 2 | 415 85 |
| HDPSF03 | 969536 | 327 | HMMER 2.1.1 | PFAM: ATPases associated with various cellular activities (AAA) | PF00004 | 47.2 | 61 | 399 |
| | | | blastx.14 | LON1 protease [Zea mays] | gi 1816586 gb AAC50011.1 | 58% 62% 41% 36% 30% | 46 865 622 580 642 | 447 1200 846 636 710 |
| HLHST63 | 581528 | 328 | HMMER 2.1.1 | PFAM: Ras family | PF00071 | 30.6 | 213 | 85 |
| HFAAJ44 | 489201 | 329 | HMMER 2.1.1 | PFAM: Rhomboid family | PF01694 | 49.5 | 6 | 299 |
| HSLEM44 | 506604 | 330 | HMMER 2.1.1 | PFAM: AcrB/AcrD/AcrF family | PF00873 | 137.4 | 2 | 256 |
| HETCL79 | 522826 | 331 | HMMER 2.1.1 | PFAM: PDZ domain (Also known as DHR or GLGF) | PF00595 | 28.1 | 242 | 457 |
| HFTAR20 | 670041 | 332 | HMMER 2.1.1 | PFAM: Glypican | PF01153 | 170.7 | 12 | 308 |
| HCUF32 | 699379 | 333 | HMMER 2.1.1 | PFAM: PDZ domain | PF00595 | 29.3 | 124 | 369 |

| | | | 2.1.1 | (Also known as DHR or GLGF). | | | | |
|---------|--------|-----|-------------|---|--------------------|------|------|-----|
| HKAEO39 | 705332 | 334 | HMMER 2.1.1 | PFAM: PDZ domain (Also known as DHR or GLGF). | PF00595 | 25.7 | 239 | 430 |
| HLWBR95 | 734474 | 335 | HMMER 2.1.1 | PFAM: PDZ domain (Also known as DHR or GLGF). | PF00595 | 46.8 | 270 | 434 |
| HPWCJ63 | 772553 | 336 | HMMER 2.1.1 | PFAM: DedA family | PF00597 | 228 | 235 | 717 |
| | | | blastx.2 | (AE000391) orf, hypothetical protein [Escherichia coli] | gb AAC76130.1 | 100% | 148 | 807 |
| HPWCJ63 | 957495 | 618 | HMMER 2.1.1 | PFAM: DedA family | PF00597 | 228 | 1152 | 670 |
| | | | blastx.2 | (AE000391) orf, hypothetical protein [Escherichia coli] | gb AAC76130.1 | 100% | 144 | 803 |
| HBXCM35 | 782911 | 337 | HMMER 2.1.1 | PFAM: PDZ domain (Also known as DHR or GLGF). | PF00595 | 27.5 | 251 | 397 |
| HULBN83 | 857836 | 338 | HMMER 2.1.1 | PFAM: PDZ domain (Also known as DHR or GLGF). | PF00595 | 38 | 133 | 363 |
| HAGET77 | 885265 | 339 | HMMER 2.1.1 | PFAM: Ezrin/radixin/moesin family | PF00769 | 37.6 | 770 | 841 |
| HMSOZ55 | 910911 | 340 | HMMER 2.1.1 | PFAM: PDZ domain (Also known as DHR or GLGF). | PF00595 | 66.7 | 276 | 500 |
| | | | blastx.14 | (AF090136) lin-7-C | gi 3885834 gb AAC7 | 89% | 3 | 500 |

| | | | | | | | | |
|---------|--------|-----|----------------|--|-------------------------------|--|-------------------------------------|--|
| HAPOR42 | 911292 | 341 | HMMER 2.1.1 | [Rattus norvegicus] PFAM: PDZ domain (Also known as DHR or GLGF). | 8075.1 PF00595 | 74% | 461 | 589 |
| | | | blastx.14 | (AF061262) semaF cytoplasmic domain associated protein 2 [Mus musculus] | gi 3851518 gb AAC7 2310.1 | 88% 83% 80% 50% | 249 679 968 1009 | 644 966 1012 1050 |
| HMVAU10 | 911449 | 342 | HMMER 2.1.1 | PFAM: PDZ domain (Also known as DHR or GLGF). | PF00595 | 68.6 | 140 | 394 |
| HTTFY29 | 911454 | 343 | HMMER 2.1.1 | PFAM: PDZ domain (Also known as DHR or GLGF). | PF00595 | 101 | 180 | 428 |
| | | | blastx.14 | (AF034746) LNXp70 [Mus musculus] | gi 3041881 gb AAC4 0076.1 | 55% 58% 34% 60% 26% 32% | 150 3 258 552 255 99 | 467 146 422 626 413 173 |
| HHFJY06 | 911456 | 344 | HMMER 2.1.1 | PFAM: PDZ domain (Also known as DHR or GLGF). | PF00595 | 59.7 | 99 | 326 |
| | | | blastx.14 | (AJ001320) multi PDZ domain protein 1 [Rattus norvegicus] | gi 2959979 emb CAA 04681.1 | 40% 29% | 132 427 | 359 519 |
| HPCIK72 | 911459 | 345 | HMMER 2.1.1 | PFAM: PDZ domain (Also known as DHR or GLGF). | PF00595 | 72 | 36 | 260 |
| | | | blastx.14 | neuroendocrine-dlg [Homo sapiens] | gi 1515355 gb AAB6 1453.1 | 58% 48% 43% | 180 180 15 | 266 260 110 |

| | | | | | | | | | |
|---------|--------|-----|-------------|--|---------------------------|--|-------|------|------|
| HFIDT84 | 919878 | 346 | HMMER 2.1.1 | PFAM: PDZ domain (Also known as DHR or GLGF). | PF00595 | | 40% | 105 | 179 |
| | | | blastx.14 | (AF034746) LNXp70 [Mus musculus] | gi 3041881 gb AAC40076.1 | | 33% | 21 | 110 |
| | | | | | | | 45% | 36 | 95 |
| | | | | | | | 40% | 114 | 179 |
| | | | | | | | 225.5 | 1879 | 2127 |
| HMCAV88 | 924874 | 347 | HMMER 2.1.1 | PFAM: PDZ domain (Also known as DHR or GLGF). | PF00595 | | 70.4 | 235 | 471 |
| | | | blastx.14 | (AL110228) hypothetical protein [Homo sapiens] | gi 5817167 emb CAB53685.1 | | 41% | 232 | 471 |
| | | | | | | | 37% | 574 | 645 |
| | | | | | | | 48.9 | 1041 | 805 |
| | | | | | | | 99% | 1107 | 487 |
| HKAIPT3 | 928809 | 348 | HMMER 2.1.1 | PFAM: PDZ domain (Also known as DHR or GLGF). | PF00595 | | 349.2 | 123 | 680 |
| | | | blastx.14 | (AF131809) Unknown [Homo sapiens] | gi 4406642 gb AAD20049.1 | | 88% | 256 | 1455 |
| | | | | | | | 91% | 1774 | 2151 |
| | | | | | | | 82% | 1462 | 1782 |
| | | | | | | | 30% | 1462 | 1728 |
| HFVHV40 | 945849 | 349 | HMMER 2.1.1 | PFAM: Adaptor complexes medium subunit family | PF00928 | | 34% | 1597 | 1779 |
| | | | blastx.14 | (AF034746) LNXp70 [Mus musculus] | gi 3041881 gb AAC40076.1 | | 29% | 1876 | 2121 |
| | | | | | | | 50% | 895 | 1002 |
| | | | | | | | 25% | 1183 | 1422 |
| | | | | | | | 26% | 1570 | 1728 |
| HMCAV88 | 924874 | 347 | HMMER 2.1.1 | PFAM: PDZ domain (Also known as DHR or GLGF). | PF00595 | | 57% | 808 | 849 |
| | | | blastx.14 | (AL110228) hypothetical protein [Homo sapiens] | gi 5817167 emb CAB53685.1 | | 50% | 1504 | 1545 |
| | | | | | | | 36% | 1507 | 1596 |
| | | | | | | | 70.4 | 235 | 471 |
| | | | | | | | 41% | 232 | 471 |
| HKAIPT3 | 928809 | 348 | HMMER 2.1.1 | PFAM: PDZ domain (Also known as DHR or GLGF). | PF00595 | | 37% | 574 | 645 |
| | | | blastx.14 | (AF131809) Unknown [Homo sapiens] | gi 4406642 gb AAD20049.1 | | 48.9 | 1041 | 805 |
| | | | | | | | 99% | 1107 | 487 |
| | | | | | | | 349.2 | 123 | 680 |
| | | | | | | | 88% | 256 | 1455 |

| | | | | | | | | |
|---------|--------|-----|----------------|--|-------------------------------|-------|-----|------|
| HTJN180 | 952231 | 350 | blastx.2 | clathrin-associated protein [Mus musculus] | gb AAA37244.1 | 98% | 108 | 680 |
| | | | HMMER 2.1.1 | PFAM: PDZ domain (Also known as DHR or GLGF). | PF00595 | 27.1 | 92 | 316 |
| HEAAE08 | 959970 | 351 | HMMER 2.1.1 | PFAM: PDZ domain (Also known as DHR or GLGF). | PF00595 | 78.5 | 277 | 516 |
| | | | blastx.14 | (AF090133) lin-7-A [Rattus norvegicus] | gi 3885828 gb AAC7 8072.1 | 96% | 223 | 612 |
| HDPLU91 | 963199 | 352 | HMMER 2.1.1 | PFAM: GNS1/SUR4 family | PF01151 | 27.2 | 452 | 550 |
| | | | blastx.2 | (AL034374) dJ483K16.1 (novel protein) [Homo sapiens] | emb CAB41293.1 | 100% | 305 | 700 |
| HAPRM21 | 963200 | 353 | HMMER 2.1.1 | PFAM: GNS1/SUR4 family | PF01151 | 43.3 | 244 | 378 |
| | | | blastx.14 | (AL034374) dJ483K16.1 (novel protein) [Homo sapiens] | gi 4680391 emb CAB 41293.1 | 100% | 1 | 630 |
| HTDAB30 | 965320 | 354 | HMMER 2.1.1 | PFAM: Adaptor complexes medium subunit family | PF00928 | 493.4 | 81 | 896 |
| H2CBN90 | 966919 | 355 | HMMER 2.1.1 | PFAM: PDZ domain (Also known as DHR or GLGF). | PF00595 | 62.4 | 609 | 821 |
| | | | blastx.14 | (AB005549) atypical PKC specific binding protein [Rattus norvegicus] | gi 3868778 dbj BAA3 4216.1 | 78% | 6 | 821 |
| HETFJ47 | 971305 | 356 | HMMER 2.1.1 | PFAM: Adaptor complexes medium | PF00928 | 797.6 | 75 | 1325 |

| | | | | blastx.14 | subunit family (AF020797) AP-mu chain family member mu1B [Homo sapiens] | gi 4587714 gb AAD2 5870.1 AF020797_1 | 99% 100% | 60 1155 | 950 1328 |
|---------|--------|-----|----------------|----------------|--|---|-------------|------------|-------------|
| HADEX52 | 971351 | 357 | HMMER 2.1.1 | HMMER 2.1.1 | PFAM: PDZ domain (Also known as DHR or GLGF). | PF00595 | 63.3 | 134 | 388 |
| HTADZ74 | 811489 | 358 | HMMER 2.1.1 | HMMER 2.1.1 | PFAM: TIR domain | PF01582 | 53.1 | 305 | 538 |
| HAPNZ77 | 887072 | 359 | HMMER 2.1.1 | HMMER 2.1.1 | PFAM: TIR domain | PF01582 | 31.9 | 292 | 483 |
| HELD74 | 963001 | 360 | HMMER 2.1.1 | HMMER 2.1.1 | PFAM: TIR domain | PF01582 | 46.5 | 492 | 779 |
| HDPLJ22 | 859915 | 361 | HMMER 2.1.1 | blastx.2 | (AF113795) toll/interleukin-1 receptor 8 [Mus musculus] | gb AAF26200.1 AF1 13795_1 | 74% | 201 | 1223 |
| HPMLD11 | 890204 | 362 | HMMER 2.1.1 | HMMER 2.1.1 | PFAM: Cullin family | PF00888 | 39.1 | 86 | 409 |
| HMVDZ78 | 938574 | 363 | HMMER 2.1.1 | HMMER 2.1.1 | PFAM: Scavenger receptor cysteine-rich domain | PF00530 | 119.6 | 57 | 350 |
| HTSFJ40 | 722406 | 364 | HMMER 2.1.1 | HMMER 2.1.1 | PFAM: IPT/TIG domain | PF01833 | 52.6 | 104 | 244 |
| HEMBZ62 | 742551 | 365 | HMMER 2.1.1 | HMMER 2.1.1 | PFAM: GTPase of unknown function | PF01926 | 37.5 | 96 | 356 |
| HHFGZ38 | 785591 | 366 | HMMER 2.1.1 | HMMER 2.1.1 | PFAM: GTPase of unknown function | PF01926 | 42.4 | 23 | 175 |
| HDPLN70 | 854010 | 367 | HMMER 2.1.1 | HMMER 2.1.1 | PFAM: WH1 domain | PF00568 | 97.2 | 338 | 799 |
| | | | | | | | 33.1 | 400 | 573 |

| | | | | | | | | |
|---------|--------|-----|----------------|---|-------------------------------|---|--|---|
| HSDJH12 | 876344 | 368 | HMMER 2.1.1 | PFAM: GTPase of unknown function | PF01926 | 115.7 | 207 | 572 |
| HNBUT01 | 913838 | 369 | HMMER 2.1.1 | PFAM: GTPase of unknown function | PF01926 | 149.3 | 30 | 503 |
| | | | blastx.14 | (AL035632) BACN32G11.d [Drosophila melanogaster] | gi 4481810 emb CAB 38462.1 | 71% 36% | 30 768 | 506 824 |
| HEOQN14 | 923752 | 370 | HMMER 2.1.1 | PFAM: GTPase of unknown function | PF01926 | 33.9 | 927 | 562 |
| | | | blastx.14 | (AC002510) unknown protein [Arabidopsis thaliana] | gi 2618702 gb AAB8 4349.1 | 54% | 951 | 787 |
| HTXKL86 | 928194 | 371 | HMMER 2.1.1 | PFAM: GTPase of unknown function | PF01926 | 133.3 | 10 | 636 |
| | | | blastx.14 | similar to hypothetical proteins [Bacillus subtilis] | gi 2633977 emb CAB 13478.1 | 37% 33% 54% 31% 30% | 4 493 334 229 355 | 219 690 405 285 444 |
| | | | HMMER 2.1.1 | PFAM: WH1 domain | PF00568 | 140.5 | 132 | 458 |
| | | | blastx.14 | ena-VASP like protein [Mus musculus] | gi 1644453 gb AAC5 2862.1 | 97% 78% 91% 27% 35% 26% 38% | 135 771 1215 751 1266 1035 880 | 539 1157 1358 879 1316 1148 933 |
| HE8TM80 | 955022 | 373 | HMMER 2.1.1 | PFAM: GTPase of unknown function | PF01926 | 51.1 | 460 | 624 |
| | | | blastx.14 | similar to GTP-binding protein; cDNA EST 111 | gi 3878119 emb CAA 88860.1 | 59% 55% | 463 4 | 624 90 |

| | | | | | | | | |
|---------|--------|-----|-----------------------------|---|------------------------------|-------------------|--------------------|--------------------|
| HWLEY40 | 957875 | 374 | HMMER 2.1.1 blastx.14 | this gene PFAM: GTPase of unknown function (AC002510) unknown protein [Arabidopsis thaliana] | PF01926 | 103.9 | 192 | 632 |
| HDPPD36 | 964320 | 620 | HMMER 2.1.1 blastx.14 | PFAM: WH1 domain | gi 2618702 gb AAB8 4349.1 | 54% 50% 70% | 1209 168 516 | 1373 347 575 |
| HOUBZ94 | 527876 | 376 | HMMER 2.1.1 | PFAM: Phosphotyrosine interaction domain (PTB/PID). | PF00640 | 41.1 | 7 | 129 |
| HMH32 | 550977 | 377 | HMMER 2.1.1 | PFAM: Guanine nucleotide exchange factor for Ras-like GTPases; N-terminal motif | PF00618 | 28.9 | 253 | 441 |
| HDPH43 | 573418 | 378 | HMMER 2.1.1 | PFAM: PX domain | PF00787 | 38.5 | 13 | 336 |
| HCE3W04 | 615501 | 379 | HMMER 2.1.1 | PFAM: RhoGEF domain | PF00621 | 46.1 | 535 | 804 |
| HMUBZ20 | 670393 | 380 | HMMER 2.1.1 | PFAM: PX domain | PF00787 | 48.8 | 2 | 184 |
| HDPAB51 | 685665 | 381 | HMMER 2.1.1 | PFAM: RhoGAP domain | PF00620 | 114.9 | 402 | 884 |
| HPJAP28 | 686349 | 382 | HMMER 2.1.1 | PFAM: RhoGAP domain | PF00620 | 28.9 | 302 | 391 |
| HIBEC79 | 703000 | 383 | HMMER 2.1.1 | PFAM: RhoGAP domain | PF00620 | 31.2 | 308 | 99 |
| HOQBF64 | 703177 | 384 | HMMER | PFAM: Regulator of G | PF00615 | 38.9 | 48 | 167 |

| | | | | | | | | |
|---------|--------|-----|----------------|---|-------------------------------|------------|-----------|------------|
| HTEDL38 | 761609 | 385 | 2.1.1 | protein signaling domain | PF00536 | 56.3 | 256 | 441 |
| HE9HI71 | 779375 | 386 | HMMER 2.1.1 | PFAM: SAM domain (Sterile alpha motif) | PF00536 | 67.7 | 290 | 466 |
| HNFS82 | 779946 | 387 | HMMER 2.1.1 | PFAM: SAM domain (Sterile alpha motif) | PF00787 | 28.7 | 53 | 259 |
| HOUHO89 | 786548 | 388 | HMMER 2.1.1 | PFAM: RhoGEF domain | PF00621 | 56 | 463 | 750 |
| HFPBB28 | 844526 | 389 | HMMER 2.1.1 | PFAM: Domain found in bacterial signal proteins | PF00672 | 43 | 60 | 236 |
| HHEWQ61 | 876063 | 390 | HMMER 2.1.1 | PFAM: PX domain | PF00787 | 36.5 | 135 | 353 |
| HUFGH09 | 877078 | 391 | HMMER 2.1.1 | PFAM: PX domain | PF00787 | 58.6 | 363 | 638 |
| HLICA79 | 880881 | 392 | HMMER 2.1.1 | PFAM: Domain found in Dishevelled, Egl-10, and Pleckstrin | PF00610 | 79.9 | 103 | 327 |
| HSLIH01 | 884251 | 393 | HMMER 2.1.1 | PFAM: Domain found in Dishevelled, Egl-10, and Pleckstrin | PF00610 | 30.9 | 83 | 304 |
| HE9OV91 | 887364 | 394 | HMMER 2.1.1 | PFAM: SPRY domain | PF00622 | 80.6 | 313 | 633 |
| HHEDS85 | 894602 | 395 | HMMER 2.1.1 | PFAM: RhoGAP domain | PF00620 | 26.2 | 11 | 121 |
| HNTDJ68 | 899624 | 396 | HMMER 2.1.1 | PFAM: SAM domain (Sterile alpha motif) | PF00536 | 42.3 | 1375 | 1569 |
| HKAHO77 | 906671 | 397 | HMMER 2.1.1 | PFAM: RhoGAP domain | PF00620 | 24.7 | 63 | 248 |
| | | | blastx.14 | GTPASE-ACTIVATING PROTEIN [Homo | gi 2276308 emb CAB 06085.1 | 69% 95% | 64 180 | 171 248 |

| | | | | | | | | | |
|---------|--------|-----|-----------------------------|--|---------------------------|--|---|--------------------------------------|---------------------------------------|
| HTFNP84 | 909687 | 398 | HMMER 2.1.1 blastx.14 | sapiens] | | | 95% 100% 72% 81% 81% 81% | 248 417 313 497 4 481 | 319 479 366 544 36 513 |
| | | | HMMER 2.1.1 blastx.14 | PFAM: RhoGEF domain | PF00621 | | 84.7 | 70 | 405 |
| | | | HMMER 2.1.1 blastx.14 | ect2 [Mus musculus] | gi 293332 gb AAA37536.1 | | 91% 62% 100% 17% | 73 1042 27 62 | 1131 1227 56 265 |
| HDQGZ78 | 909735 | 399 | HMMER 2.1.1 blastx.14 | PFAM: RhoGEF domain | PF00621 | | 85.2 | 5 | 277 |
| | | | HMMER 2.1.1 blastx.14 | (AF038388) actin-filament binding protein Frabin [Rattus norvegicus] | gi 3342246 gb AAC27698.1 | | 93% | 5 | 442 |
| HHEMD52 | 909742 | 400 | HMMER 2.1.1 blastx.14 | PFAM: RhoGEF domain | PF00621 | | 64.3 | 1295 | 1501 |
| | | | HMMER 2.1.1 blastx.14 | (AF017369) faciogenital dysplasia protein 3 [Mus musculus] | gi 3599942 gb AAC35431.1 | | 70% 62% 100% 80% 77% | 998 854 1516 815 1573 | 1510 982 1545 844 1599 |
| HSIDQ38 | 909854 | 401 | HMMER 2.1.1 blastx.14 | PFAM: RhoGAP domain | PF00620 | | 175.6 | 270 | 686 |
| | | | HMMER 2.1.1 blastx.14 | carboxyl terminus of the predicted protein shows 1 comes from this gene; cDNA EST EMBL:D32994 comes from this gene | gi 3874826 emb CAA86318.1 | | 37% 55% 25% 33% | 381 270 654 14 | 659 350 737 67 |

| | | | | | | | | |
|---------|--------|-----|-----------------------------|--|--|-------|-----|-----|
| HSKBF02 | 909855 | 402 | HMMER 2.1.1 blastx.14 | PFAM: RhoGAP domain p115 [Homo sapiens] | PF00620 gi 840786 emb CAA5 5394.1 | 130.6 | 9 | 386 |
| | | | | | | 59% | 6 | 386 |
| | | | | | | 66% | 364 | 390 |
| HIBDE74 | 909876 | 621 | HMMER 2.1.1 blastx.14 | PFAM: RhoGEF domain (AB001770) PEM-2 [Ciona savignyi] | PF00621 gi 4107011 dbj BAA3 6290.1 | 152.7 | 44 | 604 |
| | | | | | | 58% | 428 | 628 |
| | | | | | | 41% | 161 | 421 |
| | | | | | | 33% | 29 | 127 |
| HWMAE53 | 909877 | 404 | HMMER 2.1.1 blastx.14 | PFAM: RhoGEF domain (AF132481) Ese1L protein [Mus musculus] | PF00621 gi 4378891 gb AAD1 9749.1 | 53 | 112 | 267 |
| | | | | | | 44% | 112 | 285 |
| HFXCG28 | 909961 | 405 | HMMER 2.1.1 blastx.14 | PFAM: RasGEF domain (AL080117) hypothetical protein [Homo sapiens] | PF00617 gi 5262547 emb CAB 45716.1 | 162.7 | 225 | 593 |
| | | | | | | 98% | 225 | 593 |
| | | | | | | 50% | 149 | 220 |
| HFTCU45 | 910053 | 406 | HMMER 2.1.1 blastx.14 | PFAM: RhoGEF domain Trio [Homo sapiens] | PF00621 gi 3522970 gb AAC3 4245.1 | 80.9 | 82 | 474 |
| | | | | | | 70% | 1 | 501 |
| | | | | | | 41% | 34 | 387 |
| | | | | | | 35% | 421 | 540 |
| | | | | | | 57% | 488 | 529 |
| HFTBL33 | 910055 | 407 | HMMER 2.1.1 blastx.14 | PFAM: RhoGEF domain (AF091395) Trio isoform [Homo sapiens] | PF00621 gi 3644048 gb AAC4 3042.1 | 40.3 | 223 | 387 |
| | | | | | | 60% | 199 | 483 |
| | | | | | | 61% | 31 | 207 |
| | | | | | | 52% | 703 | 840 |
| | | | | | | 67% | 586 | 687 |
| | | | | | | 33% | 598 | 786 |
| | | | | | | 42% | 334 | 483 |

| | | | | | | | | | |
|---------|--------|-----|-----------------------------|--|---------|-------------------------------|--------------------------|---------------------------|----------------------------|
| HTXJA84 | 911387 | 408 | HMMER 2.1.1 blastx.14 | PFAM: Fes/CIP4 homology domain macrophage actin- associated-tyrosine- phosphorylated protein [Mus musculus] | | | 31% 47% 35% 46% | 37 199 1128 1175 | 189 267 1187 1219 |
| HKAAW89 | 911389 | 409 | HMMER 2.1.1 | PFAM: Fes/CIP4 homology domain | PF00611 | gi 3947712 emb CAA 77027.1 | 42.2 | 101 | 373 |
| HSXDD55 | 911460 | 410 | HMMER 2.1.1 blastx.14 | PFAM: RasGEF domain similar to phorbol ester and DAG binding domain; 1 | PF00617 | gi 3876235 emb CAA 94755.1 | 88% 82% 60% | 80 592 725 | 604 726 808 |
| HUFCI64 | 911558 | 411 | HMMER 2.1.1 blastx.14 | PFAM: RhoGAP domain PFAM: RhoGAP domain | PF00620 | gi 1504026 dbj BAA1 3212.1 | 44.7 146.2 | 88 333 | 345 695 |
| HWAFT84 | 911559 | 412 | HMMER 2.1.1 blastx.14 | PFAM: RhoGAP domain similar to C.elegans protein (Z37093) [Homo sapiens] | PF00620 | gi 1504026 dbj BAA1 3212.1 | 38% 56% | 285 857 | 608 904 |
| HETCL18 | 914535 | 413 | HMMER 2.1.1 blastx.2 | PFAM: Domain found in Dishevelled, Egl-10, and Pleckstrin (AF115480) cAMP- | PF00610 | gi 1504026 dbj BAA1 3212.1 | 158 | 3 | 500 |
| | | | | | | | 87% 50% | 3 8 | 773 43 |
| | | | | | | | 34.3 | 34 | 135 |
| | | | | | | | 90% | 40 | 702 |
| | | | | | | | 79.9 | 16 | 240 |
| | | | | | | gb AAD09132.1 | 39% | 28 | 276 |

| | | | | | | | | |
|---------|--------|-----|-----------------------------|---|--|----------------------------|-------------------------|--------------------------|
| HCRNK75 | 914536 | 414 | HMMER 2.1.1 blastx.2 | dependent Rap1 guanine- nucleotide exchange factor [Mus musculus] PFAM: Domain found in Dishevelled, Egl-10, and Pleckstrin (AF115480) cAMP- dependent Rap1 guanine- nucleotide exchange factor [Mus musculus] | PF00610 gb AAD09132.1 | 79.9 36% 35% | 2006 226 1707 | 1782 525 1790 |
| HTPFA03 | 922765 | 415 | HMMER 2.1.1 blastx.14 | PFAM: RhoGAP domain (AC004794) F02569_2 [Homo sapiens] | PF00620 gi 3184264 gb AAC1 8917.1 | 54.5 84% | 2 50 | 292 295 |
| HWADR60 | 926487 | 416 | HMMER 2.1.1 blastx.14 | PFAM: RhoGAP domain (AF003389) contains similarity to N-chimaerins [Caenorhabditis elegans] | PF00620 gi 2088864 gb AAC7 1136.1 | 148.8 33% 30% | 153 297 33 | 605 611 275 |
| HWLFJ01 | 928017 | 417 | HMMER 2.1.1 blastx.14 | PFAM: Phosphotyrosine interaction domain (PTB/PID). (AL117654) hypothetical protein [Homo sapiens] | PF00640 gi 5912247 emb CAB 56030.1 | 40.6 91% 46% 37% | 202 43 691 683 | 612 675 774 763 |
| HTXNG95 | 928577 | 418 | HMMER 2.1.1 blastx.14 | PFAM: SPRY domain zinc finger protein [Mus musculus] | PF00622 gi 406748 emb CAA5 3092.1 | 105.7 57% 54% 61% | 208 139 52 541 | 585 492 123 579 |
| HPCIG66 | 930886 | 419 | HMMER | PFAM: SPRY domain | PF00622 | 80.4 | 90 | 455 |

| | | | | | | | | |
|---------|--------|-----|-------------|--|---------------------------|------|-----|-----|
| | | | 2.1.1 | (AC007019) hypothetical protein [Arabidopsis thaliana] | gi 4417294 gb AAD20419.1 | 46% | 57 | 377 |
| | | | blastx.14 | | | 51% | 378 | 464 |
| | | | | | | 50% | 825 | 866 |
| | | | | | | 38% | 550 | 603 |
| | | | | | | 52% | 780 | 830 |
| HCRPU72 | 931140 | 420 | HMMER 2.1.1 | PFAM: RhoGAP domain | PF00620 | 94.9 | 314 | 715 |
| | | | blastx.2 | similar to human GTPase-activating protein(A49869) [Homo sapiens] | dbj BAA13442.1 | 97% | 77 | 799 |
| HE9RT95 | 934556 | 421 | HMMER 2.1.1 | PFAM: RhoGAP domain | PF00620 | 36.8 | 1 | 231 |
| | | | blastx.14 | carboxyl terminus of the predicted protein shows 1 comes from this gene; cDNA EST EMBL:D32994 comes from this gene | gi 3874826 emb CAA86318.1 | 34% | 1 | 237 |
| HFXJM13 | 935725 | 422 | HMMER 2.1.1 | PFAM: PX domain | PF00787 | 35.8 | 85 | 393 |
| | | | blastx.14 | similar to RNA recognition motif. (aka RRM, RBD, or 1 1 | gi 3879784 emb CAA93419.1 | 41% | 184 | 348 |
| | | | | | | 40% | 66 | 155 |
| HDPWU37 | 940705 | 423 | HMMER 2.1.1 | PFAM: RhoGAP domain | PF00620 | 50.2 | 3 | 116 |
| | | | blastx.14 | similar to SH3-binding protein [Homo sapiens] | gi 4826478 emb CAB42896.1 | 79% | 3 | 491 |
| | | | | | | 77% | 503 | 529 |
| | | | | | | 66% | 509 | 535 |
| HHSDL85 | 942246 | 424 | HMMER 2.1.1 | PFAM: RasGEF domain | PF00617 | 31 | 2 | 55 |

| | | | | | | | | |
|---------|--------|-----|-------------|--|---------------------------|--|--|---|
| | | | blastx.2 | (AF053308) putative guanine nucleotide releasing factor [Drosophila affinis] | gb AAC06257.1 | 50% | 2 | 472 |
| HTJMD31 | 942848 | 425 | HMMER 2.1.1 | PFAM: SPRY domain | PF00622 | 40.2 | 58 | 423 |
| | | | blastx.14 | (AL117386) putative protein [Arabidopsis thaliana] | gi 5881779 emb CAB55697.1 | 33% | 49 | 279 |
| HWADD57 | 943039 | 426 | HMMER 2.1.1 | PFAM: GTPase-activator protein for Ras-like GTPase | PF00616 | 56.1 | 212 | 343 |
| | | | blastx.14 | (AB016962) synGAP-b1 [Rattus norvegicus] | gi 4417207 dbj BAA74972.1 | 45% 69% 35% | 116 2 739 | 598 70 855 |
| HLWAH05 | 944904 | 427 | HMMER 2.1.1 | PFAM: RhoGAP domain | PF00620 | 224.3 | 470 | 925 |
| | | | blastx.2 | dJ37E16.2 (SH3-domain binding protein 1) [Homo sapiens] | emb CAB42896.1 | 96% 98% 41% 31% 26% 30% 37% 28% 26% 30% 20% 26% | 413 66 1103 1091 1091 1100 1103 733 1040 721 1046 999 | 1291 428 1249 1258 1327 1273 1228 924 1258 834 1267 1136 |
| HDPCI84 | 945527 | 428 | HMMER 2.1.1 | PFAM: RhoGAP domain | PF00620 | 103.4 | 85 | 519 |
| | | | blastx.2 | (AK001174) unnamed | dbj BAA91533.1 | 43% | 64 | 882 |

| | | | | | | | | |
|---------|--------|-----|----------------|---|---------------------------|--|---|--|
| HBXDJ07 | 946830 | 429 | HMMER 2.1.1 | protein product [Homo sapiens] PFAM: Synaptophysin / synaptoporin | PF01284 | 406.7 | 125 | 604 |
| | | | blastx.2 | synaptoporin - rat | pir JH0300 JH0300 | 90% 91% | 125 610 | 643 921 |
| HAMFD12 | 952438 | 430 | HMMER 2.1.1 | PFAM: Guanine nucleotide exchange factor for Ras-like GTPases; N-terminal motif | PF00618 | 40.7 | 3 | 77 |
| | | | blastx.14 | guanine nucleotide dissociation stimulator [Mus musculus] | gi 193573 gb AAA37714.1 | 84% | 3 | 434 |
| HFKHR40 | 952470 | 431 | HMMER 2.1.1 | PFAM: RhoGAP domain | PF00620 | 88.9 | 1376 | 1708 |
| | | | blastx.14 | carboxyl terminus of the predicted protein shows 1 comes from this gene; cDNA EST EMBL:D32994 comes from this gen | gi 3874826 emb CAA86318.1 | 46% 49% 81% 47% 37% 23% 37% 50% | 1319 1683 1583 232 1253 962 1211 643 | 1498 1865 1630 300 1324 1078 1282 696 |
| HDTAI08 | 953265 | 432 | HMMER 2.1.1 | PFAM: SAM domain (Sterile alpha motif) | PF00536 | 29.1 | 367 | 534 |
| HMKCX80 | 956254 | 433 | HMMER 2.1.1 | PFAM: PX domain | PF00787 | 47.3 | 425 | 613 |
| | | | blastx.14 | Unknown gene product [Homo sapiens] | gi 3417291 gb AAC31664.1 | 96% 68% | 613 533 | 699 607 |
| HCEMF69 | 961308 | 434 | HMMER 2.1.1 | PFAM: PX domain | PF00787 | 54.8 | 14 | 247 |

| | | | | | | | | |
|---------|--------|-----|-----------------------------|--|--|---------------------------------|---------------------------------|---------------------------------|
| HWLHF10 | 963422 | 435 | HMMER 2.1.1 blastx.14 | PFAM: RhoGAP domain | PF00620 | 121 | 640 | 975 |
| | | | | similar to SH3-binding protein [Homo sapiens] | gi 4826478 emb CAB42896.1 | 49% 43% 39% 68% 30% | 661 349 118 592 536 | 978 591 339 696 604 |
| HOEMG82 | 963855 | 436 | HMMER 2.1.1 | PFAM: IQ calmodulin-binding motif | PF00612 | 64.9 | 230 | 292 |
| HFXDR37 | 965915 | 437 | HMMER 2.1.1 blastx.14 | PFAM: PX domain (AF121862) sorting nexin 13 [Homo sapiens] | PF00787 gi 4689264 gb AAD27835.1 AF121862_1 | 39.9 35% 36% 33% | 1437 957 1002 2263 | 1189 631 928 2174 |
| HNNAS46 | 969470 | 438 | HMMER 2.1.1 blastx.14 | PFAM: PX domain (AF121858) sorting nexin 8 [Homo sapiens] | PF00787 gi 4689256 gb AAD27831.1 AF121858_1 | 70.2 99% 99% | 232 770 136 | 573 1435 768 |
| HRAAS26 | 971219 | 439 | HMMER 2.1.1 blastx.14 | PFAM: PX domain (AF139461) hypothetical protein SBB131 [Homo sapiens] | PF00787 gi 4894946 gb AAD32668.1 AF139461_1 | 52.9 100% | 89 59 | 367 499 |
| HHEEL28 | 973096 | 440 | HMMER 2.1.1 blastx.14 | PFAM: GTPase-activator protein for Ras-like GTPase (AF047711) nGAP [Homo sapiens] | PF00616 gi 4105589 gb AAD04814.1 | 47.4 51% | 148 4 | 372 375 |
| HCETF22 | 973324 | 441 | HMMER 2.1.1 | PFAM: Diacylglycerol kinase catalytic domain (presumed) | PF00781 | 202.1 | 112 | 468 |

| | | | | | | | | |
|---------|--------|-----|----------------|---|---------|------|-----|-----|
| HCMSF55 | 975280 | 623 | HMMER 2.1.1 | PFAM: PDZ domain (Also known as DHR or GLGF). | PF00595 | 69.3 | 154 | 393 |
|---------|--------|-----|----------------|---|---------|------|-----|-----|

[60] Table 2 further characterizes certain encoded polypeptides of the invention, by providing the results of comparisons to protein and protein family databases. The first column provides a unique clone identifier, "Clone ID NO:", corresponding to a cDNA clone disclosed in Table 1A. The second column provides the unique contig identifier, "Contig ID:" which allows correlation with the information in Table 1A. The third column provides the sequence identifier, "SEQ ID NO:", for the contig polynucleotide sequences. The fourth column provides the analysis method by which the homology/identity disclosed in the Table was determined. The fifth column provides a description of the PFAM/NR hit identified by each analysis. Column six provides the accession number of the PFAM/NR hit disclosed in the fifth column. Column seven, score/percent identity, provides a quality score or the percent identity, of the hit disclosed in column five. Comparisons were made between polypeptides encoded by polynucleotides of the invention and a non-redundant protein database (herein referred to as "NR"), or a database of protein families (herein referred to as "PFAM"), as described below.

[61] The NR database, which comprises the NBRF PIR database, the NCBI GenPept database, and the SIB SwissProt and TrEMBL databases, was made non-redundant using the computer program nrdb2 (Warren Gish, Washington University in Saint Louis). Each of the polynucleotides shown in Table 1A, column 3 (e.g., SEQ ID NO:X or the 'Query' sequence) was used to search against the NR database. The computer program BLASTX was used to compare a 6-frame translation of the Query sequence to the NR database (for information about the BLASTX algorithm please see Altshul et al., J. Mol. Biol. 215:403-410 (1990); and Gish and States, Nat. Genet. 3:266-272 (1993). A description of the sequence that is most similar to the Query sequence (the highest scoring 'Subject') is shown in column five of Table 2 and the database accession number for that sequence is provided in column six. The highest scoring 'Subject' is reported in Table 2 if (a) the estimated probability that the match occurred by chance alone is less than $1.0e-07$, and (b) the match was not to a known repetitive element. BLASTX returns alignments of short polypeptide segments of the Query and Subject sequences which share a high degree of similarity; these segments are known as High-Scoring Segment Pairs or HSPs. Table 2 reports the degree of similarity between the Query and the Subject for each HSP as a percent identity in Column 7. The percent identity is determined by dividing the number of exact matches between the two aligned sequences in the HSP, dividing by the number of Query amino acids in the HSP and multiplying by 100.

The polynucleotides of SEQ ID NO:X which encode the polypeptide sequence that generates an HSP are delineated by columns 8 and 9 of Table 2.

[62] The PFAM database, PFAM version 2.1, (Sonnhammer et al., Nucl. Acids Res., 26:320-322, 1998)) consists of a series of multiple sequence alignments; one alignment for each protein family. Each multiple sequence alignment is converted into a probability model called a Hidden Markov Model, or HMM, that represents the position-specific variation among the sequences that make up the multiple sequence alignment (see, e.g., Durbin et al., *Biological sequence analysis: probabilistic models of proteins and nucleic acids*, Cambridge University Press, 1998 for the theory of HMMs). The program HMMER version 1.8 (Sean Eddy, Washington University in Saint Louis) was used to compare the predicted protein sequence for each Query sequence (SEQ ID NO:Y in Table 1A) to each of the HMMs derived from PFAM version 2.1. A HMM derived from PFAM version 2.1 was said to be a significant match to a polypeptide of the invention if the score returned by HMMER 1.8 was greater than 0.8 times the HMMER 1.8 score obtained with the most distantly related known member of that protein family. The description of the PFAM family which shares a significant match with a polypeptide of the invention is listed in column 5 of Table 2, and the database accession number of the PFAM hit is provided in column 6. Column 7 provides the score returned by HMMER version 1.8 for the alignment. Columns 8 and 9 delineate the polynucleotides of SEQ ID NO:X which encode the polypeptide sequence which show a significant match to a PFAM protein family.

[63] As mentioned, columns 8 and 9 in Table 2, "NT From" and "NT To", delineate the polynucleotides of "SEQ ID NO:X" that encode a polypeptide having a significant match to the PFAM/NR database as disclosed in the fifth column. In one embodiment, the invention provides a protein comprising, or alternatively consisting of, a polypeptide encoded by the polynucleotides of SEQ ID NO:X delineated in columns 8 and 9 of Table 2. Also provided are polynucleotides encoding such proteins, and the complementary strand thereto.

[64] The nucleotide sequence SEQ ID NO:X and the translated SEQ ID NO:Y are sufficiently accurate and otherwise suitable for a variety of uses well known in the art and described further below. For instance, the nucleotide sequences of SEQ ID NO:X are useful for designing nucleic acid hybridization probes that will detect nucleic acid sequences contained in SEQ ID NO:X or the cDNA contained in Clone ID NO:Z. These probes will also hybridize to nucleic acid molecules in biological samples, thereby enabling immediate applications in chromosome mapping, linkage analysis, tissue identification and/or typing,

and a variety of forensic and diagnostic methods of the invention. Similarly, polypeptides identified from SEQ ID NO:Y may be used to generate antibodies which bind specifically to these polypeptides, or fragments thereof, and/or to the polypeptides encoded by the cDNA clones identified in, for example, Table 1A.

[65] Nevertheless, DNA sequences generated by sequencing reactions can contain sequencing errors. The errors exist as misidentified nucleotides, or as insertions or deletions of nucleotides in the generated DNA sequence. The erroneously inserted or deleted nucleotides cause frame shifts in the reading frames of the predicted amino acid sequence. In these cases, the predicted amino acid sequence diverges from the actual amino acid sequence, even though the generated DNA sequence may be greater than 99.9% identical to the actual DNA sequence (for example, one base insertion or deletion in an open reading frame of over 1000 bases).

[66] Accordingly, for those applications requiring precision in the nucleotide sequence or the amino acid sequence, the present invention provides not only the generated nucleotide sequence identified as SEQ ID NO:X, and a predicted translated amino acid sequence identified as SEQ ID NO:Y, but also a sample of plasmid DNA containing cDNA Clone ID NO:Z (deposited with the ATCC on October 5, 2000, and receiving ATCC designation numbers PTA 2574 and PTA 2575; deposited with the ATCC on January 5, 2001, and having depositor reference numbers TS-1, TS-2, AC-1, and AC-2; and/or as set forth, for example, in Table 1A, 6 and 7). The nucleotide sequence of each deposited clone can readily be determined by sequencing the deposited clone in accordance with known methods. Further, techniques known in the art can be used to verify the nucleotide sequences of SEQ ID NO:X.

[67] The predicted amino acid sequence can then be verified from such deposits. Moreover, the amino acid sequence of the protein encoded by a particular clone can also be directly determined by peptide sequencing or by expressing the protein in a suitable host cell containing the deposited human cDNA, collecting the protein, and determining its sequence.

RACE Protocol For Recovery of Full-Length Genes

[68] Partial cDNA clones can be made full-length by utilizing the rapid amplification of cDNA ends (RACE) procedure described in Frohman, M.A., et al., Proc. Nat'l. Acad. Sci. USA, 85:8998-9002 (1988). A cDNA clone missing either the 5' or 3' end can be reconstructed to include the absent base pairs extending to the translational start or stop codon, respectively. In some cases, cDNAs are missing the start codon of translation,

therefor. The following briefly describes a modification of this original 5' RACE procedure. Poly A+ or total RNA is reverse transcribed with Superscript II (Gibco/BRL) and an antisense or complementary primer specific to the cDNA sequence. The primer is removed from the reaction with a Microcon Concentrator (Amicon). The first-strand cDNA is then tailed with dATP and terminal deoxynucleotide transferase (Gibco/BRL). Thus, an anchor sequence is produced which is needed for PCR amplification. The second strand is synthesized from the dA-tail in PCR buffer, Taq DNA polymerase (Perkin-Elmer Cetus), an oligo-dT primer containing three adjacent restriction sites (XhoI, SalI and ClaI) at the 5' end and a primer containing just these restriction sites. This double-stranded cDNA is PCR amplified for 40 cycles with the same primers as well as a nested cDNA-specific antisense primer. The PCR products are size-separated on an ethidium bromide-agarose gel and the region of gel containing cDNA products the predicted size of missing protein-coding DNA is removed. cDNA is purified from the agarose with the Magic PCR Prep kit (Promega), restriction digested with XhoI or SalI, and ligated to a plasmid such as pBluescript SKII (Stratagene) at XhoI and EcoRV sites. This DNA is transformed into bacteria and the plasmid clones sequenced to identify the correct protein-coding inserts. Correct 5' ends are confirmed by comparing this sequence with the putatively identified homologue and overlap with the partial cDNA clone. Similar methods known in the art and/or commercial kits are used to amplify and recover 3' ends.

[69] Several quality-controlled kits are commercially available for purchase. Similar reagents and methods to those above are supplied in kit form from Gibco/BRL for both 5' and 3' RACE for recovery of full length genes. A second kit is available from Clontech which is a modification of a related technique, SLIC (single-stranded ligation to single-stranded cDNA), developed by Dumas et al., *Nucleic Acids Res.*, 19:5227-32 (1991). The major differences in procedure are that the RNA is alkaline hydrolyzed after reverse transcription and RNA ligase is used to join a restriction site-containing anchor primer to the first-strand cDNA. This obviates the necessity for the dA-tailing reaction which results in a polyT stretch that is difficult to sequence past.

[70] An alternative to generating 5' or 3' cDNA from RNA is to use cDNA library double-stranded DNA. An asymmetric PCR-amplified antisense cDNA strand is synthesized with an antisense cDNA-specific primer and a plasmid-anchored primer. These primers are removed and a symmetric PCR reaction is performed with a nested cDNA-specific antisense primer and the plasmid-anchored primer.

RNA Ligase Protocol For Generating The 5' or 3' End Sequences To Obtain Full Length Genes

[71] Once a gene of interest is identified, several methods are available for the identification of the 5' or 3' portions of the gene which may not be present in the original cDNA plasmid. These methods include, but are not limited to, filter probing, clone enrichment using specific probes and protocols similar and identical to 5' and 3' RACE. While the full length gene may be present in the library and can be identified by probing, a useful method for generating the 5' or 3' end is to use the existing sequence information from the original cDNA to generate the missing information. A method similar to 5' RACE is available for generating the missing 5' end of a desired full-length gene. (This method was published by Fromont-Racine et al., *Nucleic Acids Res.*, 21(7):1683-1684 (1993)). Briefly, a specific RNA oligonucleotide is ligated to the 5' ends of a population of RNA presumably containing full-length gene RNA transcript and a primer set containing a primer specific to the ligated RNA oligonucleotide and a primer specific to a known sequence of the gene of interest, is used to PCR amplify the 5' portion of the desired full length gene which may then be sequenced and used to generate the full length gene. This method starts with total RNA isolated from the desired source, poly A RNA may be used but is not a prerequisite for this procedure. The RNA preparation may then be treated with phosphatase if necessary to eliminate 5' phosphate groups on degraded or damaged RNA which may interfere with the later RNA ligase step. The phosphatase if used is then inactivated and the RNA is treated with tobacco acid pyrophosphatase in order to remove the cap structure present at the 5' ends of messenger RNAs. This reaction leaves a 5' phosphate group at the 5' end of the cap cleaved RNA which can then be ligated to an RNA oligonucleotide using T4 RNA ligase. This modified RNA preparation can then be used as a template for first strand cDNA synthesis using a gene specific oligonucleotide. The first strand synthesis reaction can then be used as a template for PCR amplification of the desired 5' end using a primer specific to the ligated RNA oligonucleotide and a primer specific to the known sequence of the gene of interest. The resultant product is then sequenced and analyzed to confirm that the 5' end sequence belongs to the relevant gene.

[72] The present invention also relates to vectors or plasmids which include such DNA sequences, as well as the use of the DNA sequences. The material deposited with the ATCC (deposited with the ATCC on October 5, 2000, and receiving ATCC designation numbers

PTA 2574 and PTA 2575; deposited with the ATCC on January 5, 2001, and receiving ATCC designation numbers TS-1, TS-2, AC-1, and AC-2; and/or as set forth, for example, in Table 1A, Table 6, or Table 7) is a mixture of cDNA clones derived from a variety of human tissue and cloned in either a plasmid vector or a phage vector, as described, for example, in Table 7. These deposits are referred to as "the deposits" herein. The tissues from which some of the clones were derived are listed in Table 7, and the vector in which the corresponding cDNA is contained is also indicated in Table 7. The deposited material includes cDNA clones corresponding to SEQ ID NO:X described, for example, in Table 1A (Clone ID NO:Z). A clone which is isolatable from the ATCC Deposits by use of a sequence listed as SEQ ID NO:X, may include the entire coding region of a human gene or in other cases such clone may include a substantial portion of the coding region of a human gene. Furthermore, although the sequence listing may in some instances list only a portion of the DNA sequence in a clone included in the ATCC Deposits, it is well within the ability of one skilled in the art to sequence the DNA included in a clone contained in the ATCC Deposits by use of a sequence (or portion thereof) described in, for example Tables 1A or 2 by procedures hereinafter further described, and others apparent to those skilled in the art.

[73] Also provided in Table 7 is the name of the vector which contains the cDNA clone. Each vector is routinely used in the art. The following additional information is provided for convenience.

[74] Vectors Lambda Zap (U.S. Patent Nos. 5,128,256 and 5,286,636), Uni-Zap XR (U.S. Patent Nos. 5,128, 256 and 5,286,636), Zap Express (U.S. Patent Nos. 5,128,256 and 5,286,636), pBluescript (pBS) (Short, J. M. et al., *Nucleic Acids Res.* 16:7583-7600 (1988); Altling-Mees, M. A. and Short, J. M., *Nucleic Acids Res.* 17:9494 (1989)) and pBK (Altling-Mees, M. A. et al., *Strategies* 5:58-61 (1992)) are commercially available from Stratagene Cloning Systems, Inc., 11011 N. Torrey Pines Road, La Jolla, CA, 92037. pBS contains an ampicillin resistance gene and pBK contains a neomycin resistance gene. Phagemid pBS may be excised from the Lambda Zap and Uni-Zap XR vectors, and phagemid pBK may be excised from the Zap Express vector. Both phagemids may be transformed into *E. coli* strain XL-1 Blue, also available from Stratagene.

[75] Vectors pSport1, pCMVSPORT 1.0, pCMVSPORT 2.0 and pCMVSPORT 3.0, were obtained from Life Technologies, Inc., P. O. Box 6009, Gaithersburg, MD 20897. All Sport vectors contain an ampicillin resistance gene and may be transformed into *E. coli* strain DH10B, also available from Life Technologies. See, for instance, Gruber, C. E., et al., *Focus*

15:59- (1993). Vector lafmid BA (Bento Soares, Columbia University, New York, NY) contains an ampicillin resistance gene and can be transformed into *E. coli* strain XL-1 Blue. Vector pCR[®]2.1, which is available from Invitrogen, 1600 Faraday Avenue, Carlsbad, CA 92008, contains an ampicillin resistance gene and may be transformed into *E. coli* strain DH10B, available from Life Technologies. See, for instance, Clark, J. M., *Nuc. Acids Res.* 16:9677-9686 (1988) and Mead, D. *et al.*, *Bio/Technology* 9: (1991).

[76] The present invention also relates to the genes corresponding to SEQ ID NO:X, SEQ ID NO:Y, and/or the deposited clone (Clone ID NO:Z). The corresponding gene can be isolated in accordance with known methods using the sequence information disclosed herein. Such methods include preparing probes or primers from the disclosed sequence and identifying or amplifying the corresponding gene from appropriate sources of genomic material.

[77] Also provided in the present invention are allelic variants, orthologs, and/or species homologs. Procedures known in the art can be used to obtain full-length genes, allelic variants, splice variants, full-length coding portions, orthologs, and/or species homologs of genes corresponding to SEQ ID NO:X or the complement thereof, polypeptides encoded by genes corresponding to SEQ ID NO:X or the complement thereof, and/or the cDNA contained in Clone ID NO:Z, using information from the sequences disclosed herein or the clones deposited with the ATCC. For example, allelic variants and/or species homologs may be isolated and identified by making suitable probes or primers from the sequences provided herein and screening a suitable nucleic acid source for allelic variants and/or the desired homologue.

[78] The polypeptides of the invention can be prepared in any suitable manner. Such polypeptides include isolated naturally occurring polypeptides, recombinantly produced polypeptides, synthetically produced polypeptides, or polypeptides produced by a combination of these methods. Means for preparing such polypeptides are well understood in the art.

[79] The polypeptides may be in the form of the secreted protein, including the mature form, or may be a part of a larger protein, such as a fusion protein (see below). It is often advantageous to include an additional amino acid sequence which contains secretory or leader sequences, pro-sequences, sequences which aid in purification, such as multiple histidine residues, or an additional sequence for stability during recombinant production.

[80] The polypeptides of the present invention are preferably provided in an isolated form, and preferably are substantially purified. A recombinantly produced version of a polypeptide, including the secreted polypeptide, can be substantially purified using techniques described herein or otherwise known in the art, such as, for example, by the one-step method described in Smith and Johnson, Gene 67:31-40 (1988). Polypeptides of the invention also can be purified from natural, synthetic or recombinant sources using techniques described herein or otherwise known in the art, such as, for example, antibodies of the invention raised against the polypeptides of the present invention in methods which are well known in the art.

[81] The present invention provides a polynucleotide comprising, or alternatively consisting of, the nucleic acid sequence of SEQ ID NO:X, and/or the cDNA sequence contained in Clone ID NO:Z. The present invention also provides a polypeptide comprising, or alternatively, consisting of, the polypeptide sequence of SEQ ID NO:Y, a polypeptide encoded by SEQ ID NO:X or a complement thereof, a polypeptide encoded by the cDNA contained in Clone ID NO:Z, and/or the polypeptide sequence encoded by a nucleotide sequence in SEQ ID NO:B as defined in column 6 of Table 1B. Polynucleotides encoding a polypeptide comprising, or alternatively consisting of the polypeptide sequence of SEQ ID NO:Y, a polypeptide encoded by SEQ ID NO:X, a polypeptide encoded by the cDNA contained in Clone ID NO:Z, and/or a polypeptide sequence encoded by a nucleotide sequence in SEQ ID NO:B as defined in column 6 of Table 1B are also encompassed by the invention. The present invention further encompasses a polynucleotide comprising, or alternatively consisting of, the complement of the nucleic acid sequence of SEQ ID NO:X, a nucleic acid sequence encoding a polypeptide encoded by the complement of the nucleic acid sequence of SEQ ID NO:X, and/or the cDNA contained in Clone ID NO:Z.

[82] Moreover, representative examples of polynucleotides of the invention comprise, or alternatively consist of, one, two, three, four, five, six, seven, eight, nine, ten, or more of the sequences delineated in Table 1B column 6, or any combination thereof. Additional, representative examples of polynucleotides of the invention comprise, or alternatively consist of, one, two, three, four, five, six, seven, eight, nine, ten, or more of the complementary strand(s) of the sequences delineated in Table 1B column 6, or any combination thereof. In further embodiments, the above-described polynucleotides of the invention comprise, or alternatively consist of, sequences delineated in Table 1B, column 6, and have a nucleic acid sequence which is different from that of the BAC fragment having the sequence disclosed in

SEQ ID NO:B (see Table 1B, column 5). In additional embodiments, the above-described polynucleotides of the invention comprise, or alternatively consist of, sequences delineated in Table 1B, column 6, and have a nucleic acid sequence which is different from that published for the BAC clone identified as BAC ID NO:A (see Table 1B, column 4). In additional embodiments, the above-described polynucleotides of the invention comprise, or alternatively consist of, sequences delineated in Table 1B, column 6, and have a nucleic acid sequence which is different from that contained in the BAC clone identified as BAC ID NO:A (see Table 1B, column 4). Polypeptides encoded by these polynucleotides, other polynucleotides that encode these polypeptides, and antibodies that bind these polypeptides are also encompassed by the invention. Additionally, fragments and variants of the above-described polynucleotides and polypeptides are also encompassed by the invention.

[83] Further, representative examples of polynucleotides of the invention comprise, or alternatively consist of, one, two, three, four, five, six, seven, eight, nine, ten, or more of the sequences delineated in column 6 of Table 1B which correspond to the same Clone ID NO:Z (see Table 1B, column 1), or any combination thereof. Additional, representative examples of polynucleotides of the invention comprise, or alternatively consist of, one, two, three, four, five, six, seven, eight, nine, ten, or more of the complementary strand(s) of the sequences delineated in column 6 of Table 1B which correspond to the same Clone ID NO:Z (see Table 1B, column 1), or any combination thereof. In further embodiments, the above-described polynucleotides of the invention comprise, or alternatively consist of, sequences delineated in column 6 of Table 1B which correspond to the same Clone ID NO:Z (see Table 1B, column 1) and have a nucleic acid sequence which is different from that of the BAC fragment having the sequence disclosed in SEQ ID NO:B (see Table 1B, column 5). In additional embodiments, the above-described polynucleotides of the invention comprise, or alternatively consist of, sequences delineated in column 6 of Table 1B which correspond to the same Clone ID NO:Z (see Table 1B, column 1) and have a nucleic acid sequence which is different from that published for the BAC clone identified as BAC ID NO:A (see Table 1B, column 4). In additional embodiments, the above-described polynucleotides of the invention comprise, or alternatively consist of, sequences delineated in column 6 of Table 1B which correspond to the same Clone ID NO:Z (see Table 1B, column 1) and have a nucleic acid sequence which is different from that contained in the BAC clone identified as BAC ID NO:A (see Table 1B, column 4). Polypeptides encoded by these polynucleotides, other polynucleotides that encode these polypeptides, and antibodies that bind these polypeptides

are also encompassed by the invention. Additionally, fragments and variants of the above-described polynucleotides and polypeptides are also encompassed by the invention.

[84] Further, representative examples of polynucleotides of the invention comprise, or alternatively consist of, one, two, three, four, five, six, seven, eight, nine, ten, or more of the sequences delineated in column 6 of Table 1B which correspond to the same contig sequence identifier SEQ ID NO:X (see Table 1B, column 2), or any combination thereof. Additional, representative examples of polynucleotides of the invention comprise, or alternatively consist of, one, two, three, four, five, six, seven, eight, nine, ten, or more of the complementary strand(s) of the sequences delineated in column 6 of Table 1B which correspond to the same contig sequence identifier SEQ ID NO:X (see Table 1B, column 2), or any combination thereof. In further embodiments, the above-described polynucleotides of the invention comprise, or alternatively consist of, sequences delineated in column 6 of Table 1B which correspond to the same contig sequence identifier SEQ ID NO:X (see Table 1B, column 2) and have a nucleic acid sequence which is different from that of the BAC fragment having the sequence disclosed in SEQ ID NO:B (see Table 1B, column 5). In additional embodiments, the above-described polynucleotides of the invention comprise, or alternatively consist of, sequences delineated in column 6 of Table 1B which correspond to the same contig sequence identifier SEQ ID NO:X (see Table 1B, column 2) and have a nucleic acid sequence which is different from that published for the BAC clone identified as BAC ID NO:A (see Table 1B, column 4). In additional embodiments, the above-described polynucleotides of the invention comprise, or alternatively consist of, sequences delineated in column 6 of Table 1B which correspond to the same contig sequence identifier SEQ ID NO:X (see Table 1B, column 2) and have a nucleic acid sequence which is different from that contained in the BAC clone identified as BAC ID NO:A (See Table 1B, column 4). Polypeptides encoded by these polynucleotides, other polynucleotides that encode these polypeptides, and antibodies that bind these polypeptides are also encompassed by the invention. Additionally, fragments and variants of the above-described polynucleotides and polypeptides are also encompassed by the invention.

[85] Moreover, representative examples of polynucleotides of the invention comprise, or alternatively consist of, one, two, three, four, five, six, seven, eight, nine, ten, or more of the sequences delineated in the same row of Table 1B column 6, or any combination thereof. Additional, representative examples of polynucleotides of the invention comprise, or alternatively consist of, one, two, three, four, five, six, seven, eight, nine, ten, or more of the

complementary strand(s) of the sequences delineated in the same row of Table 1B column 6, or any combination thereof. In preferred embodiments, the polynucleotides of the invention comprise, or alternatively consist of, one, two, three, four, five, six, seven, eight, nine, ten, or more of the complementary strand(s) of the sequences delineated in the same row of Table 1B column 6, wherein sequentially delineated sequences in the table (i.e. corresponding to those exons located closest to each other) are directly contiguous in a 5' to 3' orientation. In further embodiments, above-described polynucleotides of the invention comprise, or alternatively consist of, sequences delineated in the same row of Table 1B, column 6, and have a nucleic acid sequence which is different from that of the BAC fragment having the sequence disclosed in SEQ ID NO:B (see Table 1B, column 5). In additional embodiments, the above-described polynucleotides of the invention comprise, or alternatively consist of, sequences delineated in the same row of Table 1B, column 6, and have a nucleic acid sequence which is different from that published for the BAC clone identified as BAC ID NO:A (see Table 1B, column 4). In additional embodiments, the above-described polynucleotides of the invention comprise, or alternatively consist of, sequences delineated in the same row of Table 1B, column 6, and have a nucleic acid sequence which is different from that contained in the BAC clone identified as BAC ID NO:A (see Table 1B, column 4). Polypeptides encoded by these polynucleotides, other polynucleotides that encode these polypeptides, and antibodies that bind these polypeptides are also encompassed by the invention.

[86] In additional specific embodiments, polynucleotides of the invention comprise, or alternatively consist of, one, two, three, four, five, six, seven, eight, nine, ten, or more of the sequences delineated in column 6 of Table 1B, and the polynucleotide sequence of SEQ ID NO:X (e.g., as defined in Table 1B, column 2) or fragments or variants thereof. Polypeptides encoded by these polynucleotides, other polynucleotides that encode these polypeptides, and antibodies that bind these polypeptides are also encompassed by the invention.

[87] In additional specific embodiments, polynucleotides of the invention comprise, or alternatively consist of, one, two, three, four, five, six, seven, eight, nine, ten, or more of the sequences delineated in column 6 of Table 1B which correspond to the same Clone ID NO:Z (see Table 1B, column 1), and the polynucleotide sequence of SEQ ID NO:X (e.g., as defined in Table 1A or 1B) or fragments or variants thereof. In preferred embodiments, the delineated sequence(s) and polynucleotide sequence of SEQ ID NO:X correspond to the same Clone ID NO:Z. Polypeptides encoded by these polynucleotides, other polynucleotides

that encode these polypeptides, and antibodies that bind these polypeptides are also encompassed by the invention.

[88] In further specific embodiments, polynucleotides of the invention comprise, or alternatively consist of, one, two, three, four, five, six, seven, eight, nine, ten, or more of the sequences delineated in the same row of column 6 of Table 1B, and the polynucleotide sequence of SEQ ID NO:X (e.g., as defined in Table 1A or 1B) or fragments or variants thereof. In preferred embodiments, the delineated sequence(s) and polynucleotide sequence of SEQ ID NO:X correspond to the same row of column 6 of Table 1B. Polypeptides encoded by these polynucleotides, other polynucleotides that encode these polypeptides, and antibodies that bind these polypeptides are also encompassed by the invention.

[89] In additional specific embodiments, polynucleotides of the invention comprise, or alternatively consist of a polynucleotide sequence in which the 3' 10 polynucleotides of one of the sequences delineated in column 6 of Table 1B and the 5' 10 polynucleotides of the sequence of SEQ ID NO:X are directly contiguous. Nucleic acids which hybridize to the complement of these 20 contiguous polynucleotides under stringent hybridization conditions or alternatively, under lower stringency conditions, are also encompassed by the invention. Polypeptides encoded by these polynucleotides and/or nucleic acids, other polynucleotides and/or nucleic acids that encode these polypeptides, and antibodies that bind these polypeptides are also encompassed by the invention. Additionally, fragments and variants of the above-described polynucleotides, nucleic acids, and polypeptides are also encompassed by the invention.

[90] In additional specific embodiments, polynucleotides of the invention comprise, or alternatively consist of, a polynucleotide sequence in which the 3' 10 polynucleotides of one of the sequences delineated in column 6 of Table 1B and the 5' 10 polynucleotides of a fragment or variant of the sequence of SEQ ID NO:X are directly contiguous. Nucleic acids which hybridize to the complement of these 20 contiguous polynucleotides under stringent hybridization conditions or alternatively, under lower stringency conditions, are also encompassed by the invention. Polypeptides encoded by these polynucleotides and/or nucleic acids, other polynucleotides and/or nucleic acids encoding these polypeptides, and antibodies that bind these polypeptides are also encompassed by the invention. Additionally, fragments and variants of the above-described polynucleotides, nucleic acids, and polypeptides are also encompassed by the invention.

[91] In specific embodiments, polynucleotides of the invention comprise, or alternatively consist of, a polynucleotide sequence in which the 3' 10 polynucleotides of the sequence of SEQ ID NO:X and the 5' 10 polynucleotides of the sequence of one of the sequences delineated in column 6 of Table 1B are directly contiguous. Nucleic acids which hybridize to the complement of these 20 contiguous polynucleotides under stringent hybridization conditions or alternatively, under lower stringency conditions, are also encompassed by the invention. Polypeptides encoded by these polynucleotides and/or nucleic acids, other polynucleotides and/or nucleic acids encoding these polypeptides, and antibodies that bind these polypeptides are also encompassed by the invention. Additionally, fragments and variants of the above-described polynucleotides, nucleic acids, and polypeptides are also encompassed by the invention.

[92] In specific embodiments, polynucleotides of the invention comprise, or alternatively consist of, a polynucleotide sequence in which the 3' 10 polynucleotides of a fragment or variant of the sequence of SEQ ID NO:X and the 5' 10 polynucleotides of the sequence of one of the sequences delineated in column 6 of Table 1B are directly contiguous. Nucleic acids which hybridize to the complement of these 20 contiguous polynucleotides under stringent hybridization conditions or alternatively, under lower stringency conditions, are also encompassed by the invention. Polypeptides encoded by these polynucleotides and/or nucleic acids, other polynucleotides and/or nucleic acids encoding these polypeptides, and antibodies that bind these polypeptides are also encompassed by the invention. Additionally, fragments and variants of the above-described polynucleotides, nucleic acids, and polypeptides, are also encompassed by the invention.

[93] In further specific embodiments, polynucleotides of the invention comprise, or alternatively consist of, a polynucleotide sequence in which the 3' 10 polynucleotides of one of the sequences delineated in column 6 of Table 1B and the 5' 10 polynucleotides of another sequence in column 6 are directly contiguous. Nucleic acids which hybridize to the complement of these 20 contiguous polynucleotides under stringent hybridization conditions or alternatively, under lower stringency conditions, are also encompassed by the invention. Polypeptides encoded by these polynucleotides and/or nucleic acids, other polynucleotides and/or nucleic acids encoding these polypeptides, and antibodies that bind these polypeptides are also encompassed by the invention. Additionally, fragments and variants of the above-described polynucleotides, nucleic acids, and polypeptides are also encompassed by the invention.

[94] In specific embodiments, polynucleotides of the invention comprise, or alternatively consist of, a polynucleotide sequence in which the 3' 10 polynucleotides of one of the sequences delineated in column 6 of Table 1B and the 5' 10 polynucleotides of another sequence in column 6 corresponding to the same Clone ID NO:Z (see Table 1B, column 1) are directly contiguous. Nucleic acids which hybridize to the complement of these 20 lower stringency conditions, are also encompassed by the invention. Polypeptides encoded by these polynucleotides and/or nucleic acids, other polynucleotides and/or nucleic acids encoding these polypeptides, and antibodies that bind these polypeptides are also encompassed by the invention. Additionally, fragments and variants of the above-described polynucleotides, nucleic acids, and polypeptides are also encompassed by the invention.

[95] In specific embodiments, polynucleotides of the invention comprise, or alternatively consist of, a polynucleotide sequence in which the 3' 10 polynucleotides of one sequence in column 6 corresponding to the same contig sequence identifier SEQ ID NO:X (see Table 1B, column 2) are directly contiguous. Nucleic acids which hybridize to the complement of these 20 contiguous polynucleotides under stringent hybridization conditions or alternatively, under lower stringency conditions, are also encompassed by the invention. Polypeptides encoded by these polynucleotides and/or nucleic acids, other polynucleotides and/or nucleic acids encoding these polypeptides, and antibodies that bind these polypeptides are also encompassed by the invention. Additionally, fragments and variants of the above-described polynucleotides, nucleic acids, and polypeptides are also encompassed by the invention.

[96] In specific embodiments, polynucleotides of the invention comprise, or alternatively consist of a polynucleotide sequence in which the 3' 10 polynucleotides of one of the sequences delineated in column 6 of Table 1B and the 5' 10 polynucleotides of another sequence in column 6 corresponding to the same row are directly contiguous. In preferred embodiments, the 3' 10 polynucleotides of one of the sequences delineated in column 6 of Table 1B is directly contiguous with the 5' 10 polynucleotides of the next sequential exon delineated in Table 1B, column 6. Nucleic acids which hybridize to the complement of these 20 contiguous polynucleotides under stringent hybridization conditions or alternatively, under lower stringency conditions, are also encompassed by the invention. Polypeptides encoded by these polynucleotides and/or nucleic acids, other polynucleotides and/or nucleic acids encoding these polypeptides, and antibodies that bind these polypeptides are also

encompassed by the invention. Additionally, fragments and variants of the above-described polynucleotides, nucleic acids, and polypeptides are also encompassed by the invention.

[97] Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. Accordingly, for each contig sequence (SEQ ID NO:X) listed in the fourth column of Table 1A, preferably excluded are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 and the final nucleotide minus 15 of SEQ ID NO:X, b is an integer of 15 to the final nucleotide of SEQ ID NO:X, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:X, and where b is greater than or equal to a + 14. More specifically, preferably excluded are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a and b are integers as defined in columns 4 and 5, respectively, of Table 3. In specific embodiments, the polynucleotides of the invention do not consist of at least one, two, three, four, five, ten, or more of the specific polynucleotide sequences referenced by the Genbank Accession No. as disclosed in column 6 of Table 3 (including for example, published sequence in connection with a particular BAC clone). In further embodiments, preferably excluded from the invention are the specific polynucleotide sequence(s) contained in the clones corresponding to at least one, two, three, four, five, ten, or more of the available material having the accession numbers identified in the sixth column of this Table (including for example, the actual sequence contained in an identified BAC clone). In no way is this listing meant to encompass all of the sequences which may be excluded by the general formula, it is just a representative example. All references available through these accessions are hereby incorporated by reference in their entirety.

TABLE 3

| Clone ID NO: Z | SEQ ID NO: X | Contig ID: | EST Disclaimer Range of a Range of b | | Accession #'s |
|-------------------|-----------------------|---------------|--|-----------|---|
| HDPTE21 | 11 | 1165861 | 1 - 4732 | 15 - 4746 | |
| H6EDR51 | 12 | 1197894 | 1 - 2300 | 15 - 2314 | |
| HAPRA41 | 13 | 1154054 | 1 - 1264 | 15 - 1278 | |
| HBXBI07 | 14 | 1171958 | 1 - 339 | 15 - 353 | |
| HBXCM38 | 15 | 910086 | 1 - 2160 | 15 - 2174 | AI752485, AI804792, AI439106, AI971133, AI991958, AI752484, AI432296, AI478420, AW082819, AI912373, R89026, AA894797, AI554161, AI752414, H13307, AI249165, R61527, N62403, R89727, N47856, AI689339, AI368569, R61583, AI984780, AA219502, H44175, AI802627, AI752415, T32963, AW295386, AA985168, H06745, R40750, M79099, AA203312, R00511, A91842, A91846, A91844, and A91848. |
| HCE3E50 | 16 | 1227586 | 1 - 3775 | 15 - 3789 | |
| HCEQD04 | 17 | 1150868 | 1 - 625 | 15 - 639 | |
| HDPHI92 | 18 | 909900 | 1 - 2933 | 15 - 2947 | AC068341. |
| HDPLT89 | 19 | 962403 | 1 - 2437 | 15 - 2451 | |
| HDPSU48 | 20 | 1228284 | 1 - 2902 | 15 - 2916 | |
| HDPWE80 | 21 | 909916 | 1 - 932 | 15 - 946 | |
| HDQFY84 | 22 | 1092137 | 1 - 3253 | 15 - 3267 | |
| HEONQ19 | 23 | 930705 | 1 - 897 | 15 - 911 | |
| HFCBB56 | 24 | 910073 | 1 - 553 | 15 - 567 | AA339423, and AC068296. |
| HFKKZ94 | 25 | 1163070 | 1 - 1318 | 15 - 1332 | |
| HHBGJ53 | 26 | 1187668 | 1 - 388 | 15 - 402 | |
| HHFJF24 | 27 | 1212624 | 1 - 2787 | 15 - 2801 | |
| HHFMM10 | 28 | 1178801 | 1 - 1857 | 15 - 1871 | |
| HHPBA42 | 29 | 901921 | 1 - 899 | 15 - 913 | |
| HHSP89 | 30 | 1217052 | 1 - 2277 | 15 - 2291 | |
| HKABX13 | 31 | 1167182 | 1 - 970 | 15 - 984 | |
| HLTHG77 | 32 | 1162409 | 1 - 392 | 15 - 406 | |
| HLWBZ09 | 33 | 1179714 | 1 - 1940 | 15 - 1954 | |
| HLWEH54 | 34 | 1227713 | 1 - 4510 | 15 - 4524 | |
| HLYAA41 | 35 | 1188029 | 1 - 797 | 15 - 811 | |
| HLYDV62 | 36 | 1154065 | 1 - 805 | 15 - 819 | |
| HMCFB47 | 37 | 1151498 | 1 - 796 | 15 - 810 | |
| HMSOI20 | 38 | 1178817 | 1 - 2431 | 15 - 2445 | |
| HOENH55 | 39 | 1163460 | 1 - 612 | 15 - 626 | |
| HPIAI01 | 40 | 1078178 | 1 - 926 | 15 - 940 | |
| HPJCT50 | 41 | 1201773 | 1 - 1983 | 15 - 1997 | |
| HPMFE91 | 42 | 1164740 | 1 - 1867 | 15 - 1881 | |
| HRAED51 | 43 | 1090522 | 1 - 645 | 15 - 659 | |
| HSMBA19 | 44 | 1197925 | 1 - 2252 | 15 - 2266 | |
| HSYCY88 | 45 | 914775 | 1 - 1128 | 15 - 1142 | |
| HTEDW26 | 46 | 909749 | 1 - 1158 | 15 - 1172 | |
| HTEKD92 | 47 | 1090524 | 1 - 1447 | 15 - 1461 | |
| HTLDT05 | 48 | 1227127 | 1 - 2672 | 15 - 2686 | |
| HTPDS90 | 49 | 1197926 | 1 - 1920 | 15 - 1934 | |
| HTPHM71 | 50 | 1194698 | 1 - 2017 | 15 - 2031 | |
| HUUAR12 | 51 | 1194702 | 1 - 1704 | 15 - 1718 | |
| HWAGP22 | 52 | 1150195 | 1 - 1716 | 15 - 1730 | |

| | | | | | |
|---------|----|---------|----------|-----------|---|
| HWBCE37 | 53 | 906968 | 1 - 418 | 15 - 432 | |
| HWLFB60 | 54 | 1223499 | 1 - 2867 | 15 - 2881 | |
| HDPGS16 | 55 | 1075725 | 1 - 447 | 15 - 461 | |
| HDQDV69 | 56 | 937850 | 1 - 837 | 15 - 851 | AA887783, AW392670, U46341, AL119457, AL119341, AW372827, U46346, AW384394, AW363220, AL119484, AL119497, AL119355, AL119319, AL119324, AL119443, Z99396, U46350, U46351, AL119363, AL119391, AL119444, AL134902, U46347, U46349, AL119483, AL119396, AL134528, AL119418, AL119335, AL119496, AL119439, AL042433, AL119522, AL042965, AL134524, AL119399, AL134920, AL037205, AL119401, U46345, AL134536, AI142132, AL119464, AL042450, AL042614, AL043029, AL134525, AL134538, AI142131, AL042551, AL042984, AL042975, AL042544, AL043019, AL042970, AI142134, AL042542, AL043003, AL119488, AF169035, AF085233, AB026436, AR054110, A81671, AR066494, AR060234, and AR069079. |
| HE6BK63 | 57 | 1153879 | 1 - 755 | 15 - 769 | |
| HFKDR14 | 58 | 974255 | 1 - 1721 | 15 - 1735 | AI761729, AW162515, AW104395, AW298361, AI073443, N40162, AI832126, AI827518, AW297353, R52045, AI342317, R71958, AF128625, AF021936, and AB032950. |
| HFPER82 | 59 | 1152249 | 1 - 619 | 15 - 633 | |
| HAAAO58 | 60 | 1091088 | 1 - 1309 | 15 - 1323 | |
| HADFK69 | 61 | 1091937 | 1 - 1603 | 15 - 1617 | |
| HDPMO62 | 62 | 1152329 | 1 - 1123 | 15 - 1137 | |
| HDPMO85 | 63 | 1228282 | 1 - 2479 | 15 - 2493 | |
| HDPUY72 | 64 | 1228285 | 1 - 3040 | 15 - 3054 | |
| HDTJF87 | 65 | 1154640 | 1 - 826 | 15 - 840 | |
| HE8TB94 | 66 | 1178794 | 1 - 1913 | 15 - 1927 | |
| HE8UB55 | 67 | 1228113 | 1 - 3332 | 15 - 3346 | |
| HEBGA65 | 68 | 1178633 | 1 - 1803 | 15 - 1817 | |
| HEGBB59 | 69 | 1197907 | 1 - 2465 | 15 - 2479 | |
| HELHC48 | 70 | 956003 | 1 - 803 | 15 - 817 | |
| HEOQH90 | 71 | 1212646 | 1 - 2609 | 15 - 2623 | |
| HFKHA18 | 72 | 1152242 | 1 - 1055 | 15 - 1069 | |
| HFKMA10 | 73 | 964258 | 1 - 960 | 15 - 974 | |
| HHBFM91 | 74 | 1092116 | 1 - 901 | 15 - 915 | |
| HIBBF63 | 75 | 912715 | 1 - 950 | 15 - 964 | AC012171, AC012171, AC012171, AC009065, AC009065, AC009065, AC005346, AC005346, and AC005346. |
| HMCEI38 | 76 | 1134410 | 1 - 613 | 15 - 627 | |
| HMWJD68 | 77 | 1154790 | 1 - 1350 | 15 - 1364 | |
| HOEOL58 | 78 | 1078090 | 1 - 778 | 15 - 792 | |
| HRACA51 | 79 | 1162856 | 1 - 1075 | 15 - 1089 | |
| HSHAV32 | 80 | 1180388 | 1 - 2589 | 15 - 2603 | |
| HTPDE66 | 81 | 971281 | 1 - 479 | 15 - 493 | |
| HTPDV73 | 82 | 997659 | 1 - 411 | 15 - 425 | |
| HTPHE33 | 83 | 1163871 | 1 - 1714 | 15 - 1728 | |
| HUFDN58 | 84 | 1224609 | 1 - 2404 | 15 - 2418 | |
| HUVFX92 | 85 | 1225329 | 1 - 428 | 15 - 442 | |

| | | | | | |
|---------|----|---------|----------|-----------|---|
| HWAEG71 | 86 | 1182321 | 1 - 1471 | 15 - 1485 | |
| HWAHD49 | 87 | 1228064 | 1 - 1365 | 15 - 1379 | |
| HWLGG31 | 88 | 1178825 | 1 - 2007 | 15 - 2021 | |
| HWLKF25 | 89 | 1089052 | 1 - 1097 | 15 - 1111 | |
| H2CBH45 | 90 | 963811 | 1 - 470 | 15 - 484 | AA307462, AA036880, AL133047, D89677, AC068243, and AC068243. |
| HAGDN53 | 91 | 1092161 | 1 - 1702 | 15 - 1716 | |
| HAMFM39 | 92 | 971347 | 1 - 4593 | 15 - 4607 | AI951619, AI814592, AI745391, AI922346, AA426190, AW105735, AW297557, AI829867, AI971865, AA227834, AW028756, AA151872, AA757072, AI202419, AW176248, AW295401, AI659079, AA149658, AA425159, AI765117, AI870033, AW194075, AA233413, AW102818, R61588, AA365664, AA365663, AA601170, R61532, AA357346, AA551861, AI660231, AI467782, Z99396, AW392670, AL119324, AL119319, U46350, U46351, AL119457, AL119484, AL119391, U46347, AW372827, AL119522, AL119439, AL119335, AW384394, AL119483, AW363220, AL119363, AL119497, U46349, AL119355, AL119444, AL119443, U46341, AL134518, AL134525, AL119341, AL037205, AL119401, U46346, AL119396, AL134538, AL134531, AL134528, AL119418, AL119496, AL119399, U46345, AL134524, AL042544, AL042614, AL042984, AL042542, AL043019, AL042450, AL134542, AL043003, AL042965, AL042975, AL043029, AL042551, AL119464, I05430, I05393, A10617, AR028792, AR028791, AR028793, I25027, AR054109, I44515, I26928, I26930, I26927, I25041, I44516, A01324, AR035224, AR009151, I85513, AR009152, A01323, AR027099, AR034783, A94046, A94054, I63120, AR067733, AR064322, AR064323, AR064320, AR064321, A32110, A94048, A94061, A49045, AR038321, A83642, AR019094, A83643, A70359, A92666, AR038307, A92668, A92667, I49890, A92665, A92081, A92080, A92077, A92078, A92079, AR018924, AR018923, A48774, A48775, AR000006, AR015960, AR015961, AR000007, A91752, A91751, AR051652, A85308, AR068508, AR068510, AR068509, I91969, A91754, I58322, I58323, AR003585, A63067, A51047, A63064, A63072, AR031375, AR068507, A60213, AR068506, AR062871, A44171, AR068550, A23373, AR068551, A49700, A60207, A60208, A29109, A32111, I58669, A58521, AR031374, I07209, I07249, A63954, AR051651, AR019097, AR019098, AR019096, AR029417, I77227, AR020199, AR020200, AR001287, AR020198, AR020197, I89986, AR051957, AR029418, AR067734, AR067731, AR067732, Y14971, |

| | | | | | |
|----------|-----|---------|----------|-----------|---|
| | | | | | A93444, A46342, A46343, AB026436, I09121, AR032878, AR060234, AR066494, A81671, AR054110, and AR069079. |
| HBGQT03 | 93 | 908173 | 1 - 1196 | 15 - 1210 | AW193981, AA576536, AW439879, AA218860, AA587394, AI735027, AW206358, AI075695, AI749755, AI073515, AI283940, AI828816, AW328242, AA452508, AI741698, F25077, AA454093, AI280249, AI826261, AI567379, AA350150, AI251129, F26225, AI354257, AA171893, AW129660, AI357160, F26293, F36700, H24638, AI270014, AI952189, AA834233, AI689497, AI688448, F17480, Z38509, T11668, N93072, AW362737, T11669, AW273866, N93071, AW328241, AF130979, AC024045, AC024045, and AC024045. |
| HBGSJ13 | 94 | 1150790 | 1 - 808 | 15 - 822 | |
| HBIBQ89 | 95 | 909782 | 1 - 851 | 15 - 865 | AA399613, F11248, Z42117, AA082253, F05395, T35421, and AB007925. |
| HCECM90 | 96 | 945088 | 1 - 1379 | 15 - 1393 | AA463356, AA453500, AA322899, AA340682, H24259, AA603868, AA330182, R19782, and AB023227. |
| HCEPH71 | 97 | 522739 | 1 - 432 | 15 - 446 | AA326209, AA383931, AL365319, and AL390715. |
| HCFMT57 | 98 | 1175204 | 1 - 2197 | 15 - 2211 | |
| HCOMM05 | 99 | 1173146 | 1 - 1625 | 15 - 1639 | |
| HCOOZ11 | 100 | 965306 | 1 - 689 | 15 - 703 | AI350354, AI904299, AI902503, D61534, T78554, AW183962, AI218626, AW304978, W74167, AI081779, AL022238, AL137499, AL022238, AL022238, and AL022238. |
| HCWFF88 | 101 | 506577 | 1 - 304 | 15 - 318 | AL157951, AL157951, AL157951, and AC025670. |
| HDMAV01 | 102 | 1194696 | 1 - 1796 | 15 - 1810 | |
| HDPDA47 | 103 | 929193 | 1 - 1036 | 15 - 1050 | AW402583, AL049683, and AL023653. |
| HDPFF24 | 104 | 909232 | 1 - 447 | 15 - 461 | AI929099, AI566117, AI928828, N88094, AA365879, AA281290, H67457, N87549, AW450464, AA295368, AA527887, AI033615, AA354369, AA086081, and AA903373. |
| HDPP035 | 105 | 966248 | 1 - 1890 | 15 - 1904 | AI640500, AW439548, AI823872, AW297416, AA831672, AI815031, AA994323, AA741162, AA471280, AI223999, AW339548, AW235171, AI635436, AA035703, AA747998, AI371399, N67227, AA361754, AA063573, AI536057, AI357169, R33401, C01451, R33402, AA825399, AF165138, and AF130247. |
| HDPSR74 | 106 | 911396 | 1 - 709 | 15 - 723 | |
| HDTKQ14 | 107 | 886936 | 1 - 541 | 15 - 555 | AL023653, AL049683, AL359542, AL359542, and AL359542. |
| HE6GF02 | 108 | 1150897 | 1 - 790 | 15 - 804 | |
| HE8PK12 | 109 | 909884 | 1 - 707 | 15 - 721 | AA296029, AL117472, U58883, AF136380, AF136381, AF078667, and AF078666. |
| HE9SE62 | 110 | 911476 | 1 - 915 | 15 - 929 | AW021430, AI765247, AI822051, AI822104, AA010459, N70537, AL133567, and AB018312. |
| HEOPL36 | 111 | 1195682 | 1 - 2095 | 15 - 2109 | |
| HFB DJ13 | 112 | 911264 | 1 - 476 | 15 - 490 | M86084, and AF030131. |

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|---------|-----|--------|----------|-----------|---|
| HFTDF15 | 113 | 657020 | 1 - 367 | 15 - 381 | AL365277, AL365277, AL365277, AC024511, AC024511, and AC024511. |
| HHEQV39 | 114 | 932851 | 1 - 873 | 15 - 887 | AA355773, and AA355926. |
| HHFCK09 | 115 | 965304 | 1 - 2789 | 15 - 2803 | AI218626, AI076006, AW162820, AI797880, AI922744, AI872391, AI559566, AL045117, AW161046, AW162613, AI565503, AW183962, AI857802, AA460810, AI884907, AI371131, AW248493, AI081779, AA460372, AA679085, N27884, AA581796, AA074070, AA971563, AI292006, AI922373, W76538, N93245, AI609183, AW172513, AI904299, AI682939, AA075764, AI885613, AA747871, AA449042, AA928020, AW401847, AA449757, AW268637, AW073851, AW304978, AI683858, AA568598, W74167, AI367698, AW191998, N62781, AW016535, AI902503, AA347639, AA297591, AA379280, AA568887, AA649970, AW264577, AI221886, H20460, AW387087, AW000860, AI275195, AA341002, T32918, AW162711, W25103, AI699657, R42681, AW243790, AA768740, T78554, AI279653, AI560482, AI696251, AI951374, Z45830, AA147203, AI499410, R43259, AI350354, AA732831, AW079129, AA375228, F08622, AI475009, R56337, AA379846, R17163, AW380349, AA783050, AW247402, N47545, R35508, R51077, AI474934, N79729, D61534, Z41466, AI678630, AA339343, AW367003, AA160401, Z41592, AW079321, N47546, AI252528, R58857, T16943, H55297, AL022238, AL137499, and AJ236700. |
| HISDS62 | 116 | 935932 | 1 - 506 | 15 - 520 | W27339, AA126105, AA306119, W27700, AB007884, and AJ250425. |
| HLQDT35 | 117 | 839777 | 1 - 516 | 15 - 530 | AA706241, AA707183, AA152440, N99172, AA131985, AA358765, AA253107, R10421, N56752, AA290907, R08557, AA485099, AI091625, AA134742, AL137699, AC010998, AC010998, AC010998, AC013357, AC013357, and AC013357. |
| HLWFN63 | 118 | 908437 | 1 - 3089 | 15 - 3103 | AA707313, AI880426, AI684827, AI744551, AI307796, AA101249, AI284152, AA007399, N98643, AI375268, N66095, R71685, R02817, AA085724, AI221876, AI061056, AW207571, AA111956, AI460369, AI333887, AA594062, R18624, R62793, W22434, AW007868, AA776586, T70023, R71720, H70803, AA323135, AA101290, AA029721, AA320669, AI193496, R07828, AA007478, AI915644, AI932703, T69946, R62792, AA029660, AI859215, AA205667, AI625446, AI273982, AB018333, AC006599, AL033378, AL033378, AC006599, and AC006599. |
| HMEFT66 | 119 | 856149 | 1 - 337 | 15 - 351 | |
| HMSCD15 | 120 | 918133 | 1 - 1223 | 15 - 1237 | AA828277, AI707568, AI333720, W33154, AI880870, AA848014, AA864599, N50622, AW087770, AW270419, AA761244, AA262754, AA779760, AI880826, AW407353, W37119, AA206843, Z42584, |

| | | | | | |
|---------|-----|---------|----------|-----------|---|
| | | | | | AA206842, AB011126, AL158207, AL158207, and AC027008. |
| HMSHO64 | 121 | 746582 | 1 - 398 | 15 - 412 | |
| HMTAW83 | 122 | 911385 | 1 - 487 | 15 - 501 | AI908321, AA831896, AR058970, AR058968, A68194, and AR058969. |
| HMVAM09 | 123 | 963814 | 1 - 1009 | 15 - 1023 | AI685410, AI969804, AA621392, AA358533, AW135812, AI376856, and AI276887. |
| HNSAA28 | 124 | 946988 | 1 - 1544 | 15 - 1558 | AA713959, AI564093, AA768779, AA825697, AA808021, AA808149, AI401490, AW181992, AW444640, AI018159, AF146277, and AF077003. |
| HOGEQ43 | 125 | 1226207 | 1 - 4196 | 15 - 4210 | |
| HOUDH19 | 126 | 1150918 | 1 - 515 | 15 - 529 | |
| HOUFT36 | 127 | 911293 | 1 - 832 | 15 - 846 | AI806483, AI147946, AA256164, AW236751, AA057615, AW362445, AA542823, AF162130, AC005084, and AF161181. |
| HPMFL08 | 128 | 959569 | 1 - 452 | 15 - 466 | AA555286, AA640814, AI281916, AW073979, AI378363, R70468, AW242350, AW013856, AA644290, AW449140, Z93016, AC012384, AL035541, AC005228, AC003662, AC009300, and Z93016. |
| HRSMD49 | 129 | 723025 | 1 - 443 | 15 - 457 | AA136820. |
| HSDII69 | 130 | 917180 | 1 - 1612 | 15 - 1626 | AA203346, AA203330, AA489694, AI912487, AW024848, AA133454, AA640288, AA658936, Z24863, AA665267, AA878769, AI024792, AI383978, AW022618, T31809, AA318980, T86474, AA669824, AA115749, AW296909, AA552781, AI459513, AI332862, AI332863, and T86475. |
| HSDSB06 | 131 | 949151 | 1 - 2264 | 15 - 2278 | AW009631, AI765056, AA877550, AA102362, AA625117, AA447454, AA446651, AA724535, AI220147, AA430607, AA019158, AI198643, AW389353, AA516463, AW197881, AA045561, AA186967, H86071, H67029, AW378928, H12433, AA768085, R66487, AA478635, N55248, AA359925, R33870, AA385529, AA054621, AA961423, AW002948, AI802284, AA377365, D31590, AW275740, AI766068, C01179, AL133047, D89677, and AF003234. |
| HSFAM09 | 132 | 1150965 | 1 - 531 | 15 - 545 | |
| HSSAX53 | 133 | 507509 | 1 - 348 | 15 - 362 | |
| HSVAW49 | 134 | 1150960 | 1 - 970 | 15 - 984 | |
| HTEAG49 | 135 | 954614 | 1 - 1289 | 15 - 1303 | AW452652, AI039005, AA780077, AW316890, AI337290, AA463229, AA463230, AI423317, AI468158, AA382497, N66986, AF041822, AL390796, AL390796, AL357045, and AL357045. |
| HTLBH67 | 136 | 751985 | 1 - 432 | 15 - 446 | W19592, AC005368, AC008439, AC022420, AC022420, AC022420, AC005368, AC005368, AC008781, and AC008781. |
| HTLJC71 | 137 | 922923 | 1 - 1738 | 15 - 1752 | AL039539, AL045443, AI336919, AA406128, AA405229, AL042307, AA431504, AA311249, AW086440, AA813520, AI240644, AA897733, AW268487, AA782009, AW172455, AI301209, AI014598, AA969918, AL041043, AA431178, |

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| HTPAD46 | 138 | 503313 | 1 - 343 | 15 - 357 | AA386091, AA386130, AL133510, and AC010932. |
| HTTKP07 | 139 | 911390 | 1 - 562 | 15 - 576 | AI640500, AA035703, AF130247, and AF165138. |
| HUCOW17 | 140 | 933357 | 1 - 843 | 15 - 857 | W52616, AA102287, R60274, AA307147, H17000, H15631, C03464, and AA192581. |
| HWHGF52 | 141 | 726102 | 1 - 441 | 15 - 455 | AA223889, and AB002360. |
| HWHHB69 | 142 | 1212612 | 1 - 2914 | 15 - 2928 | |
| HWLFH94 | 143 | 1151387 | 1 - 1251 | 15 - 1265 | |
| HWMBM1 3 | 144 | 909683 | 1 - 858 | 15 - 872 | AI339104, AA861042, AA134985, AA868144, AA134946, AI626100, AA922724, AA535447, AA056635, AA308766, D25742, AA916634, AA551763, AA873574, AW192836, AR044148, AL158847, and AL158847. |
| HWWDN3 4 | 145 | 911357 | 1 - 1233 | 15 - 1247 | AI671062, AI023330, AW243448, AI990947, AW081367, AW391909, AA448391, AI984688, AA448394, AI283270, AI344135, AW014216, AA127530, AA335984, AA377148, Z42084, R12430, AA400585, AC019214, and AC019214. |
| HCEML27 | 146 | 997051 | 1 - 894 | 15 - 908 | |
| HELHJ69 | 147 | 1128924 | 1 - 630 | 15 - 644 | |
| HFKLA09 | 148 | 1178800 | 1 - 2072 | 15 - 2086 | |
| HSBBF79 | 149 | 965764 | 1 - 1361 | 15 - 1375 | |
| HSLKA77 | 150 | 1204269 | 1 - 4086 | 15 - 4100 | |
| HAGDR21 | 151 | 1090433 | 1 - 1414 | 15 - 1428 | |
| HHFNH27 | 152 | 1025277 | 1 - 1952 | 15 - 1966 | |
| HTLIT05 | 153 | 1217625 | 1 - 844 | 15 - 858 | |
| HAPNV33 | 154 | 1151374 | 1 - 793 | 15 - 807 | |
| HBTAE84 | 155 | 1128800 | 1 - 489 | 15 - 503 | |
| HDPVY89 | 156 | 827026 | 1 - 684 | 15 - 698 | AC026283, and AC026283. |
| HGLDB21 | 157 | 1010920 | 1 - 1670 | 15 - 1684 | |
| HMIAN37 | 158 | 947881 | 1 - 677 | 15 - 691 | |
| HODAK55 | 159 | 1110333 | 1 - 713 | 15 - 727 | |
| HSLEI59 | 160 | 1128801 | 1 - 758 | 15 - 772 | |
| HSQFH29 | 161 | 1217061 | 1 - 1907 | 15 - 1921 | |
| HTLEA35 | 162 | 1107230 | 1 - 674 | 15 - 688 | |
| HUVGG63 | 163 | 1204716 | 1 - 2211 | 15 - 2225 | |
| HAGAX57 | 164 | 1150865 | 1 - 1237 | 15 - 1251 | |
| HAMGX15 | 165 | 1177932 | 1 - 750 | 15 - 764 | |
| HAUBV06 | 166 | 1106041 | 1 - 2203 | 15 - 2217 | |
| HBWCM62 | 167 | 1185273 | 1 - 465 | 15 - 479 | |
| HCWFA35 | 168 | 1105672 | 1 - 611 | 15 - 625 | |
| HDACA35 | 169 | 1107236 | 1 - 983 | 15 - 997 | |
| HDQGM08 | 170 | 1151469 | 1 - 896 | 15 - 910 | |
| HELGB06 | 171 | 1148741 | 1 - 433 | 15 - 447 | |
| HEOPR74 | 172 | 1226822 | 1 - 1245 | 15 - 1259 | |
| HIBEK35 | 173 | 731480 | 1 - 402 | 15 - 416 | |
| HJMAR88 | 174 | 1104937 | 1 - 683 | 15 - 697 | |
| HMWGU56 | 175 | 1226470 | 1 - 1016 | 15 - 1030 | |

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| HOUDS09 | 176 | 1164010 | 1 - 1631 | 15 - 1645 | |
| HTEGM38 | 177 | 675087 | 1 - 350 | 15 - 364 | |
| HTEKY82 | 178 | 1152495 | 1 - 486 | 15 - 500 | |
| HTLCY54 | 179 | 1193550 | 1 - 1049 | 15 - 1063 | |
| HFOXK14 | 180 | 603245 | 1 - 616 | 15 - 630 | AL096870, and AL096870. |
| HHFFO69 | 181 | 837703 | 1 - 901 | 15 - 915 | |
| HHFLU06 | 182 | 857884 | 1 - 316 | 15 - 330 | AL096870, and AL096870. |
| HAGBA56 | 183 | 732597 | 1 - 653 | 15 - 667 | AA812064, AA430303, AA430200, AI803142, AI425013, AA954361, AB020641, U62391, AF033655, AC006036, AC000057, and AC002458. |
| HAGGF84 | 184 | 911312 | 1 - 421 | 15 - 435 | AL135568, AJ252239, AF071569, U73504, D14906, J05072, X63615, AC004056, and AC004168. |
| HAHGD33 | 185 | 921782 | 1 - 1051 | 15 - 1065 | AW378448, AW378426, AA064738, Z43369, AA984486, D31100, W79308, T35774, T08259, W52734, W73106, AI904952, R10018, AA348984, T80752, AA639598, R57404, T81225, AW408302, T81300, R13945, T47464, W79389, Z43504, AA404490, AA196613, W01185, H14918, H45144, and AF113249. |
| HAHIY08 | 186 | 962113 | 1 - 265 | 15 - 279 | AA100160, AA307684, AA244505, R57782, AA864846, AR044133, and AR044123. |
| HBIOZ10 | 187 | 973131 | 1 - 490 | 15 - 504 | AC010761, and AC010761. |
| HBKDI30 | 188 | 729048 | 1 - 625 | 15 - 639 | AA197072, R02824, J05194, J03886, and AL160175. |
| HBXBW40 | 189 | 706115 | 1 - 462 | 15 - 476 | AL023754, AL049688, and D86557. |
| HCEHE35 | 190 | 909937 | 1 - 378 | 15 - 392 | AB019692. |
| HCEPW85 | 191 | 911374 | 1 - 302 | 15 - 316 | N83965, AA326737, and H14153. |
| HCFAT25 | 192 | 932068 | 1 - 579 | 15 - 593 | AI287912, AL134532, AF096300, AB014587, AC005035, AL137755, and U88984. |
| HCFCF47 | 193 | 1139731 | 1 - 980 | 15 - 994 | |
| HDAAV61 | 194 | 810305 | 1 - 329 | 15 - 343 | AI762433, AI191825, AA159268, AA083866, AW105372, AA157878, AI140935, AI922109, AA158846, AA488548, AI187149, AA442140, AA837990, AI494201, AL048644, AI366974, AI537837, AA425228, AW410089, AL038605, AI821259, AW084097, AW083168, AI624304, AI918554, AA508692, AI918634, AI307494, AI349622, AI738867, AI310571, AI802372, AI918408, AW021662, AI348897, AI366959, AW058233, AI345397, AL038564, AW089275, AI340511, AA857847, AI446405, AI799305, AW022494, AW020288, AI281867, AI312210, AI307569, AI270295, N71180, AI702301, N75771, AL036652, AW021373, AL036856, AI312428, AI866820, AW059713, AI889147, N27632, AI336513, AW022102, AA019646, AI348895, AI313320, AI336495, AI310920, AI307503, AW079736, AW082532, AW089572, AI345143, AI309391, AI955906, AI309431, AI336662, AI868204, AI310575, AI349276, AI307507, N22406, AA420722, AI336565, AI683559, AL040694, AI311440, AI334893, AI349186, AI340533, AW088560, AI690472, AI521005, AI537515, AI493601, |

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| HDPKD75 | 195 | 810824 | 1 - 524 | 15 - 538 | AA923698, AL040000, AF191838, AR016417, AF191839, and AF145705. |
| HDPNC96 | 196 | 934520 | 1 - 720 | 15 - 734 | AA256100, and AB023182. |
| HDPSR15 | 197 | 969666 | 1 - 1218 | 15 - 1232 | AW195239, AW149418, AW005579, AI378013, AA147800, AI436586, AI392913, AW337924, AI377235, AI264931, AI203549, AW104319, AI094031, AA461376, H59980, AW166255, AA508841, AI360737, AA463275, AA417605, AI682196, H59937, AI208175, N30324, AA460078, AW001677, AA514325, N50317, AA741518, AI091790, T11446, AA360254, AI208678, AA214523, D20738, R61563, T12550, T11445, AA428834, AI276889, AB026289, and AR044150. |
| HDQDX20 | 198 | 919027 | 1 - 1280 | 15 - 1294 | AI905612, N75655, N94726, AA297704, H53438, AW339945, AW405560, AA719945, AI682436, AA971968, AW085268, H67340, |

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| HDQHB19 | 199 | 1226089 | 1 - 2263 | 15 - 2277 | |
| HDTBY88 | 200 | 934472 | 1 - 495 | 15 - 509 | AA868305, AI700890, AA789239, AI803004, AI694352, AA043382, F08474, R21498, AF112183, AF112184, and AC005354. |
| HE2KZ07 | 201 | 909948 | 1 - 1167 | 15 - 1181 | AI141657, AW410635, AI377644, AI373441, AI435842, AI813994, AI222162, AI816276, AA134062, AA115521, AA027340, AI198968, AI936995, AA432023, AI417110, AA019881, AA431770, T33003, AI804202, AW296590, AA894568, AA888588, AI816392, AW157195, AA774185, AI312197, AA770240, AI005469, T15996, AI589559, T83662, AI802351, AA164900, AI637808, AW294821, AI612103, AI452706, R96447, AI214546, AA083117, AI219844, AI312448, AA978205, H98210, AI423512, AA115526, N74543, AI823785, H19250, T16797, AI803155, AW051574, Z41102, AI300274, AA970855, T30646, T78862, T81921, R42142, R38428, R05531, T99321, H16697, R08035, AA114950, H52123, AA114923, R41504, R08085, F18392, D79266, R42920, AI028740, AA114993, F34433, F25527, AA130289, C02151, AL118820, AI696123, H10371, AA954386, T34819, AA135800, AI219437, T81018, AA135799, AI372829, AI056831, H68913, AW051694, AI986390, W28788, H10372, U95740, D86556, AB004267, AB023027, and AF181984. |
| HE8UY74 | 202 | 960914 | 1 - 553 | 15 - 567 | N23547, H06088, Z24919, R94366, AA010516, AA004981, AA304780, AL356968, and AL356968. |
| HE9NO66 | 203 | 974353 | 1 - 976 | 15 - 990 | AI732997, AA865818, AA977633, Z69734, AB035267, AB020741, and Z68339. |
| HEMBT61 | 204 | 939957 | 1 - 449 | 15 - 463 | N86549, AW369713, and AB002301. |
| HETLF29 | 205 | 909762 | 1 - 404 | 15 - 418 | AA960957, AI001155, and AC004664. |
| HFIUE75 | 206 | 909758 | 1 - 1104 | 15 - 1118 | AA745592, AA780791, AI680317, AA205127, R06019, AW074511, T76970, AW408392, T86065, T77135, AI709216, R05922, T85884, AA730855, and R77022. |
| HFKIT06 | 207 | 934019 | 1 - 286 | 15 - 300 | AC026976, AC068353, AC068353, AF284563, AF284563, and AC026976. |
| HHEGG20 | 208 | 894409 | 1 - 808 | 15 - 822 | AF084205. |
| HHEHC53 | 209 | 921783 | 1 - 896 | 15 - 910 | AW408302, AW410815, AW161181, AA160313, AA226860, AA044358, AI632654, AA232389, Z43369, AA249020, T35774, AA852244, AA064738, AA295773, D31100, R13945, AA205277, T47464, T08259, AI904952, AF113249, AC009427, AC009427, and AC009427. |
| HHHERQ79 | 210 | 944057 | 1 - 497 | 15 - 511 | AW340333, AI806295, AW268810, AA827664, AA829237, AA909185, |

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| | | | | | AA919008, AA604425, AW407893, AA011359, AL134902, D63485, AB016590, AB016589, and AR043113. |
| HISAF59 | 211 | 959140 | 1 - 899 | 15 - 913 | AW401787, AI394630, AI418298, AW375742, T30407, Z44281, F07299, R25015, T32685, AA974700, F07734, AA297059, AW239548, AA897415, R45025, AI807678, AI343378, AW206793, AW138409, AW163027, AI815476, AA503315, AA047793, AW137324, AW140018, AI936871, AI015047, AI017077, AI168175, AI302185, AI025217, F03423, R46686, AI073417, Z40806, AA026054, AW002416, AI652375, F03562, T03397, AI983297, H42881, T82311, AI025310, AI831833, R08769, AI911100, AA471062, AW157059, AA382959, H22172, AI356604, AI537006, AI825970, AW338394, AW192088, AI559159, AA593826, AW078709, and Z61277. |
| HKAKM10 | 212 | 918685 | 1 - 596 | 15 - 610 | AW166113, R88730, AF071071, AF170303, AF170304, AF077658, and AF071070. |
| HLTHP86 | 213 | 919354 | 1 - 2470 | 15 - 2484 | AA702160, AI457618, AI951809, AI808761, AI911971, AI808636, AI633963, AI092909, AA922021, N53171, AA809486, AI092910, AI253245, AA236950, AI432182, AI093897, AI363415, N50448, AI248799, AA663589, AA235935, AI239417, AA121162, AW270053, AI889821, AW296666, AI263508, N50504, H16878, H09671, AW028355, AW300355, R56761, H84971, AI373750, H16267, Z44040, Z44727, AI025923, N58608, T95750, T34716, AA363673, R43831, AA687486, R91239, AI829631, AA687431, AA852910, H16769, T95749, AI268135, AI686257, R56913, Z40554, AA834548, AA872305, C02338, and AF161420. |
| HMSJL96 | 214 | 934483 | 1 - 662 | 15 - 676 | R01798. |
| HMTAJ73 | 215 | 813296 | 1 - 651 | 15 - 665 | AI831613, AI924408, AI870169, AW068406, AI368905, AW168626, AI284115, AA678670, AA568895, H19069, AA627558, AA857431, AJ010119, AF074714, AF074715, AC015698, and AC015698. |
| HNTCP13 | 216 | 909770 | 1 - 1793 | 15 - 1807 | AI479379, AW273740, AA463847, AI740675, AI014722, AI922082, AA463334, AW009462, AI073540, N95224, AI190238, AA007373, AI798079, AA476563, AA670286, H02882, N92851, AA652716, AW016339, H45475, W25554, AA774170, H45576, AI370125, AI811794, AW119159, H03781, H20952, AA853882, AA853883, AI471060, AW382128, AW371996, W21053, H20991, AA368628, AW138258, AA476448, AA876335, AA788825, AF037447, and AC004486. |
| HNTMD79 | 217 | 934522 | 1 - 573 | 15 - 587 | AA305176, AL160291, AL160291, AL365228, and AL365228. |

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| HNTMH70 | 218 | 757184 | 1 - 674 | 15 - 688 | H19102, AI699883, AI383263, AC005726, and AC004807. |
| HNTNB14 | 219 | 909942 | 1 - 644 | 15 - 658 | AA082976, R60839, AA349498, F12661, T74243, L22557, AC068701, and AC068701. |
| HODFF88 | 220 | 974911 | 1 - 1843 | 15 - 1857 | D80164, D59502, D80193, D80195, D59275, C15076, D80227, D58283, D80022, D80166, D81030, D59859, D51799, D59619, D80210, D80391, D80240, D59787, D51423, D80253, D80043, D80269, D50979, D80212, D80038, D80196, D80024, D80219, D80188, C14331, D59467, D57483, D59927, D80378, D80366, C14389, D59889, D50995, D80045, D59610, AA305409, C14429, D80241, D51060, T03269, C14014, AW178893, C75259, AA305578, D81026, D59695, D51022, AW179328, D81111, AW178775, D80134, AW378532, AW177440, D51250, AW352158, D80268, F13647, AA514188, AW369651, D80251, D80522, D51079, D80248, D80949, D58253, AW178762, D80168, D52291, C14227, AA514186, AI905856, AW177501, AW177511, D80133, Z21582, AW360811, C05695, C14298, AW352117, D80064, AW176467, AW375405, AW378540, C14407, AW377671, D51097, AW366296, D80302, AW360844, AW360817, AW375406, AW378534, AW179332, AW377672, AW179023, AW178905, D80132, AW360834, AA285331, D80439, AW352171, AW377676, AW178906, AW352170, AW177731, D80247, AW178907, AW179019, AW179024, D51103, AW177505, AW360841, AW179020, AW178909, AW177456, AW179329, AW178980, AW177733, AW378528, AW178908, AW178754, AW179018, AW179220, AI557751, AW179004, AW178914, AW378525, AW352174, T11417, D80157, AW177728, D59627, D51759, AW367967, AW178774, AW178911, AW378543, AW352163, D59503, D80258, D80014, C06015, AI557774, AW178983, AW352120, T03116, AW178781, T48593, D58246, C14077, D59653, AW177723, D58101, D45260, AI525923, AW178986, AW367950, C03092, AA809122, H67854, D59551, H67866, C14975, T02974, AW378533, AW378539, D51213, AW177734, AI535686, D59317, D51221, AI525917, C14973, AA514184, C14344, D45273, AI525925, AI525920, D59474, AI525227, D31458, C14046, AI525242, AI525235, T03048, AI525912, AW378542, AI525215, AI525237, C16955, C05763, Z33452, AI535850, AI535961, A84916, AJ132110, A62300, A62298, AR018138, X67155, Y17188, D26022, A25909, A67220, D89785, A78862, D34614, D88547, AF058696, X82626, AR008278, AB028859, AR025207, I82448, Y12724, A82595, AB012117, |

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| HOHCE47 | 221 | 1216683 | 1 - 2147 | 15 - 2161 | |
| HPCRV84 | 222 | 945856 | 1 - 475 | 15 - 489 | AA307070, D79997, L76158, and X95351. |
| HRACK83 | 223 | 888037 | 1 - 566 | 15 - 580 | AC005832. |
| HRADM45 | 224 | 717358 | 1 - 468 | 15 - 482 | AA418916, AA426580, AJ271722, AP000260, AP000036, AF055919, AP000099, and AP000098. |
| HRAED74 | 225 | 942527 | 1 - 691 | 15 - 705 | AC005940, L42810, S83194, AF117384, and AB023658. |
| HRODZ70 | 226 | 942673 | 1 - 572 | 15 - 586 | AA292911, AA167655, AA167766, H97685, AA635138, Z41812, and AB007941. |
| HSKAC24 | 227 | 823869 | 1 - 498 | 15 - 512 | AF170301, AF170302, AF077659, and AF144573. |
| HSSMT34 | 228 | 911294 | 1 - 540 | 15 - 554 | AA378627, F07835, and AL117482. |
| HT3BG12 | 229 | 921593 | 1 - 368 | 15 - 382 | AB028951, and AL122055. |
| HTEGO05 | 230 | 932583 | 1 - 1086 | 15 - 1100 | AA059465, AA059211, AA731209, AA236961, T86500, T87461, AL024498, and M35862. |
| HTEKT33 | 231 | 953308 | 1 - 1648 | 15 - 1662 | AW292935, AW027321, AW027332, AI538521, AL040176, H29877, H85389, H29974, H84772, Z41499, AL045794, T24112, T24119, D80253, D80043, AI744745, AL039924, D80219, AW013814, D59275, T10477, D51250, D80240, AA016312, D80227, H00069, D80210, D51423, D80134, AL043441, T02921, D59619, D80193, AL039156, D80391, AL039150, AL043445, AL038821, D59787, AL039509, AL039564, AL039538, AL044530, AL039108, AL039678, D80196, AL039074, AL038837, AL039625, AL039648, AL039629, AL039566, D80045, AL039659, T23947, AL037726, AL038531, D80168, AL039109, AL040992, AL039128, AL044407, AL036973, AL043423, AL045337, AL037051, AL045353, AL036725, AL039386, AL039423, AL045341, AL042909, AL039410, C14227, D80366, AL043422, AL038025, D59927, T11051, D81026, AL039085, AL036196, C14014, D59889, AI535783, AW451070, D80038, C75259, D50995, C15076, AL037639, R47228, D80022, AI535983, AL037526, AL037615, D80195, D80949, D58283, |

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| HTEMU66 | 232 | 944419 | 1 - 1078 | 15 - 1092 | <p>AL039924, AL045794, AW013814, AL036630, T02921, AL044412, T24119, AL044364, T24112, AW450335, AL039476, D51250, D80253, D80043, AL040992, AL039109, AL038531, AL037726, AL039629, AL039625, AL039648, AL038837, AL039074, AL039678, AL039108, AL039538, AL039564, AL039156, AL039659, AL039566, AL039509, AL039521, H00069, AL039128, AL044407, AL036973, AL045337, AL037051, AL045353, AL039386, AL039423, AL045341, AL042909, AL039410, D59787, AL039150, AL044530, AL038821, AL038025, D80219, AL036725, AL043422, D59275, AL043445, AL039459, AI535983, D80227, AL043586, AL043423, D80240, AL043441, D80210, D51423, T23947, AL036650, D80134, AL036196, D59619, D80391, AL037639, D80193, AW451070, AL037615, D80196, AL036767, C14227, AL039085, AI535783, D80949, AL036117, D80366, D59927, AL037526, AL042334, AW452756, D80168, R47228, AL036238, AL036679, AL037601, T11051, D81026, AL039504, C14014, D50995, C75259, AL039842, AL036964, D80045, AL036733, AL036158, AL037027, AL036924, AL037054, D59889, AL036765,</p> |

AL037007

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| HTEMV09 | 233 | 909843 | 1 - 1347 | 15 - 1361 | AI818734, AA454060, AA453640, AW268879, AI377304, AI818733, AI818743, AI681535, AI741915, AA948041, AI198872, AW341578, AI267885, AA767746, AI677678, AI829855, AI677729, AW129267, AA947425, AA297313, AL041049, N67346, and AA889773. |
| HTEMV66 | 234 | 1151075 | 1 - 847 | 15 - 861 | |
| HTGAU79 | 235 | 1175071 | 1 - 2139 | 15 - 2153 | |
| HTLEJ11 | 236 | 973302 | 1 - 956 | 15 - 970 | M62294. |
| HTLIY52 | 237 | 1218691 | 1 - 1362 | 15 - 1376 | |
| HTOAK34 | 238 | 966800 | 1 - 1271 | 15 - 1285 | AW408167, AA491322, AA505126, AI340133, AA831203, N27153, AA053564, AA809481, AF181985, and AF179867. |
| HTPGG25 | 239 | 911282 | 1 - 829 | 15 - 843 | AA018361, AI768326, AI333117, AA324901, F07835, AA378627, AL117482, Z61430, AC020705, and AC020705. |
| HUJAD24 | 240 | 1161319 | 1 - 1722 | 15 - 1736 | |
| HUTSF11 | 241 | 966029 | 1 - 416 | 15 - 430 | AI384010, AI288640, Z20435, and A74523. |
| HUVGZ88 | 242 | 1227628 | 1 - 2921 | 15 - 2935 | |
| HWADY66 | 243 | 1096252 | 1 - 352 | 15 - 366 | |
| HWAFG04 | 244 | 952878 | 1 - 1646 | 15 - 1660 | AI302185, AI652375, AI936871, AW206793, |

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| HWAFS18 | 245 | 948434 | 1 - 946 | 15 - 960 | W25237, and AF156884. |
| HWAGS73 | 246 | 1150212 | 1 - 612 | 15 - 626 | |
| HWLEA48 | 247 | 927676 | 1 - 415 | 15 - 429 | AA130828, AF169034, Z98752, and AF169033. |
| HWLHS82 | 248 | 934505 | 1 - 415 | 15 - 429 | AW401390, and AC005581. |
| HWMIB81 | 249 | 955336 | 1 - 1479 | 15 - 1493 | AW380440, AW299858, AW391525, H78769, H78659, H53674, AA628987, AA447173, AW204470, AA343468, AA480342, AF155118, AC021719, and AC016143. |
| HCWDV17 | 250 | 1105673 | 1 - 684 | 15 - 698 | |
| HELDI95 | 251 | 1103374 | 1 - 983 | 15 - 997 | |
| HAGFO25 | 252 | 1150845 | 1 - 806 | 15 - 820 | |
| HAWAB54 | 253 | 1149319 | 1 - 1428 | 15 - 1442 | |
| HLIBV06 | 254 | 934887 | 1 - 2224 | 15 - 2238 | |
| HMALL66 | 255 | 1105097 | 1 - 495 | 15 - 509 | |
| HOACE12 | 256 | 858976 | 1 - 439 | 15 - 453 | |
| HOGCG69 | 257 | 924848 | 1 - 1209 | 15 - 1223 | |
| HAGAE09 | 258 | 1150864 | 1 - 838 | 15 - 852 | |
| HAGAE34 | 259 | 1121869 | 1 - 757 | 15 - 771 | |
| HARMH78 | 260 | 1137572 | 1 - 547 | 15 - 561 | |
| HBJLB53 | 261 | 1226988 | 1 - 2037 | 15 - 2051 | |
| HBJNB52 | 262 | 1128792 | 1 - 793 | 15 - 807 | |
| HDABQ83 | 263 | 1201703 | 1 - 446 | 15 - 460 | |
| HDPDC84 | 264 | 1226990 | 1 - 3243 | 15 - 3257 | |
| HDPUF40 | 265 | 1212494 | 1 - 2384 | 15 - 2398 | |
| HDPWU07 | 266 | 1228286 | 1 - 3262 | 15 - 3276 | |
| HDTJJ02 | 267 | 1106328 | 1 - 318 | 15 - 332 | |
| HE2GA18 | 268 | 1121872 | 1 - 276 | 15 - 290 | |
| HE2SY03 | 269 | 1207925 | 1 - 1070 | 15 - 1084 | |
| HELGY64 | 270 | 1228289 | 1 - 2669 | 15 - 2683 | |
| HFIYW31 | 271 | 1151476 | 1 - 1271 | 15 - 1285 | |
| HFVIP88 | 272 | 1124705 | 1 - 898 | 15 - 912 | |
| HGBAS76 | 273 | 1193040 | 1 - 1677 | 15 - 1691 | |
| HHEBB62 | 274 | 1151481 | 1 - 541 | 15 - 555 | |
| HHEHU73 | 275 | 1151483 | 1 - 1007 | 15 - 1021 | |
| HHEMA11 | 276 | 1151484 | 1 - 638 | 15 - 652 | |
| HHEQK01 | 277 | 1107392 | 1 - 622 | 15 - 636 | |
| HHPEM84 | 278 | 915639 | 1 - 360 | 15 - 374 | |
| HHSED84 | 279 | 1150832 | 1 - 760 | 15 - 774 | |
| HIBCC94 | 280 | 1161292 | 1 - 1264 | 15 - 1278 | |

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| HKADN56 | 281 | 1220254 | 1 - 3121 | 15 - 3135 | |
| HKIXG58 | 282 | 1124750 | 1 - 713 | 15 - 727 | |
| HLICI13 | 283 | 1177963 | 1 - 1856 | 15 - 1870 | |
| HLTGF17 | 284 | 662405 | 1 - 370 | 15 - 384 | |
| HLYDC50 | 285 | 1151494 | 1 - 860 | 15 - 874 | |
| HMADD49 | 286 | 1217031 | 1 - 2214 | 15 - 2228 | |
| HMEKE78 | 287 | 1128290 | 1 - 1811 | 15 - 1825 | |
| HMSHU26 | 288 | 1150833 | 1 - 1079 | 15 - 1093 | |
| HNEEB82 | 289 | 1076509 | 1 - 677 | 15 - 691 | |
| HNHIA06 | 290 | 1162086 | 1 - 710 | 15 - 724 | |
| HODFY16 | 291 | 1105244 | 1 - 797 | 15 - 811 | |
| HPQSB68 | 292 | 1221022 | 1 - 431 | 15 - 445 | |
| HRDBH04 | 293 | 1150876 | 1 - 1472 | 15 - 1486 | |
| HSICR69 | 294 | 1226965 | 1 - 1734 | 15 - 1748 | |
| HSIGJ94 | 295 | 1105417 | 1 - 701 | 15 - 715 | |
| HSYBL15 | 296 | 1104299 | 1 - 917 | 15 - 931 | |
| HTEKH29 | 297 | 855660 | 1 - 2063 | 15 - 2077 | |
| HTGEL46 | 298 | 1151520 | 1 - 1543 | 15 - 1557 | |
| HTGFA05 | 299 | 1198110 | 1 - 1736 | 15 - 1750 | |
| HTLDU61 | 300 | 1165319 | 1 - 1092 | 15 - 1106 | |
| HTOFT34 | 301 | 1152490 | 1 - 1467 | 15 - 1481 | |
| HTTDH46 | 302 | 1152491 | 1 - 1130 | 15 - 1144 | |
| HTTIO05 | 303 | 1229905 | 1 - 2571 | 15 - 2585 | |
| HWHGY45 | 304 | 911621 | 1 - 191 | 15 - 205 | AC021102. |
| HWLQR48 | 305 | 1128304 | 1 - 494 | 15 - 508 | |
| HWLQX76 | 306 | 1152280 | 1 - 453 | 15 - 467 | |
| HATDD09 | 307 | 1165331 | 1 - 1282 | 15 - 1296 | |
| HBJGT03 | 308 | 1105484 | 1 - 768 | 15 - 782 | |
| HMTMF45 | 309 | 1141737 | 1 - 773 | 15 - 787 | |
| HHPDV86 | 310 | 522953 | 1 - 666 | 15 - 680 | AL109627, AL109627, AC025928, and AC025928. |
| HE8BT56 | 311 | 732602 | 1 - 365 | 15 - 379 | |
| HUJDH06 | 312 | 907613 | 1 - 692 | 15 - 706 | |
| HOEJG61 | 313 | 907614 | 1 - 660 | 15 - 674 | |
| HE8PN24 | 314 | 907620 | 1 - 713 | 15 - 727 | |
| HGBHI37 | 315 | 909745 | 1 - 491 | 15 - 505 | |
| HCHOK82 | 316 | 909755 | 1 - 1077 | 15 - 1091 | |
| HFPCH24 | 317 | 912608 | 1 - 474 | 15 - 488 | |
| HTTKF86 | 318 | 912689 | 1 - 332 | 15 - 346 | Z82188, Z82188, and Z82188. |
| HCESA79 | 319 | 912709 | 1 - 302 | 15 - 316 | AC012171, AC012171, AC012171, AC009065, AC009065, AC009065, AC005346, AC005346, and AC005346. |
| HDTBJ28 | 320 | 912714 | 1 - 521 | 15 - 535 | AP001793, AC008052, AC008052, AC015676, AC015676, and AP000864. |
| HDPBF48 | 321 | 912783 | 1 - 945 | 15 - 959 | |
| HTPFY55 | 322 | 912928 | 1 - 562 | 15 - 576 | |
| HMSCM47 | 323 | 923632 | 1 - 711 | 15 - 725 | |
| HEOQA56 | 324 | 925132 | 1 - 413 | 15 - 427 | AC013449. |
| HTPCQ24 | 325 | 925349 | 1 - 436 | 15 - 450 | Z99716, and Z99716. |
| HWAEI37 | 326 | 929481 | 1 - 403 | 15 - 417 | AL035461, and AL035461. |
| HDPSF03 | 327 | 969536 | 1 - 1283 | 15 - 1297 | |
| HLHST63 | 328 | 581528 | 1 - 410 | 15 - 424 | |
| HFAAJ44 | 329 | 489201 | 1 - 287 | 15 - 301 | |
| HSLEM44 | 330 | 506604 | 1 - 337 | 15 - 351 | AC078913, AC022123, and AC010357. |
| HETCL79 | 331 | 522826 | 1 - 465 | 15 - 479 | |
| HFTAR20 | 332 | 670041 | 1 - 908 | 15 - 922 | |
| HCUFD32 | 333 | 699379 | 1 - 702 | 15 - 716 | |

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|---------|-----|--------|----------|-----------|---|
| HKAEO39 | 334 | 705332 | 1 - 450 | 15 - 464 | |
| HLWBR95 | 335 | 734474 | 1 - 908 | 15 - 922 | AC013252, and AC013252. |
| HPWCJ63 | 336 | 772553 | 1 - 1407 | 15 - 1421 | |
| HBXCM35 | 337 | 782911 | 1 - 578 | 15 - 592 | |
| HULBN83 | 338 | 857836 | 1 - 624 | 15 - 638 | |
| HAGET77 | 339 | 885265 | 1 - 1730 | 15 - 1744 | |
| HMSOZ55 | 340 | 910911 | 1 - 979 | 15 - 993 | AC024229, and AC024229. |
| HAPOR42 | 341 | 911292 | 1 - 1102 | 15 - 1116 | |
| HMVAU10 | 342 | 911449 | 1 - 574 | 15 - 588 | |
| HTTFY29 | 343 | 911454 | 1 - 707 | 15 - 721 | |
| HHFJY06 | 344 | 911456 | 1 - 584 | 15 - 598 | |
| HPCIK72 | 345 | 911459 | 1 - 269 | 15 - 283 | |
| HFIDT84 | 346 | 919878 | 1 - 2655 | 15 - 2669 | |
| HMCAV88 | 347 | 924874 | 1 - 1031 | 15 - 1045 | AC068231, AC068231, AC068231, AL357752, AL357752, AC005476, and AC005476. |
| HKAIP73 | 348 | 928809 | 1 - 1441 | 15 - 1455 | |
| HFVHV40 | 349 | 945849 | 1 - 668 | 15 - 682 | AC020911, AC020911, and AC020911. |
| HTJN180 | 350 | 952231 | 1 - 1017 | 15 - 1031 | |
| HEAAE08 | 351 | 959970 | 1 - 1053 | 15 - 1067 | AC008687, and AC008687. |
| HDPLU91 | 352 | 963199 | 1 - 734 | 15 - 748 | |
| HAPRM21 | 353 | 963200 | 1 - 857 | 15 - 871 | AL034374, AL034374, and AL034374. |
| HTDAB30 | 354 | 965320 | 1 - 1248 | 15 - 1262 | |
| H2CBN90 | 355 | 966919 | 1 - 809 | 15 - 823 | |
| HETFJ47 | 356 | 971305 | 1 - 1767 | 15 - 1781 | |
| HADEX52 | 357 | 971351 | 1 - 1819 | 15 - 1833 | |
| HTADZ74 | 358 | 811489 | 1 - 602 | 15 - 616 | AF077346, AC007278, and AC007278. |
| HAPNZ77 | 359 | 887072 | 1 - 469 | 15 - 483 | AC003046, AC005859, AC076973, AC003046, AC005859, AC023098, and AC023098. |
| HELDR74 | 360 | 963001 | 1 - 1414 | 15 - 1428 | AI741422, AW249482, AA573909, AA085764, AW272801, AI052311, AA151131, AI700257, AA490620, AA310938, AI683396, AI284596, AA961817, AA862960, AW073675, R87485, AI828443, AI925221, AI969547, AW001375, N24896, AI521481, AI925228, AI695515, AA609182, AA151130, AI245859, AA490809, AA040451, AW139250, AI970384, AI961068, T67610, AA923298, AA513675, AW027490, T96070, AI624751, T67494, AI936161, AW196036, AA679554, AI917354, N36317, AA302588, AI932690, AW250249, R88163, T72363, AI796143, W32439, AA582049, AI539047, W45013, and AF113795. |
| HDPLJ22 | 361 | 859915 | 1 - 533 | 15 - 547 | |
| HPMLD11 | 362 | 890204 | 1 - 1297 | 15 - 1311 | |
| HMVDZ78 | 363 | 938574 | 1 - 236 | 15 - 250 | AB002313. |
| HTSFJ40 | 364 | 722406 | 1 - 378 | 15 - 392 | W28953, H19139, R54508, H10122, H08285, AA313257, R59784, F08505, R52605, Z43765, F08180, AI401170, F05493, F07194, R13670, R13641, Z45409, AW407594, F07185, AW407965, AA461135, AA371650, AC006171, AC006171, and AL161645. |
| HEMBZ62 | 365 | 742551 | 1 - 458 | 15 - 472 | R13025. |
| HHFGZ38 | 366 | 785591 | 1 - 1153 | 15 - 1167 | AA372117, AA133546, and AI468754. |
| HDPLN70 | 367 | 854010 | 1 - 968 | 15 - 982 | |

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|---------|-----|--------|----------|-----------|---|
| HSDJH12 | 368 | 876344 | 1 - 610 | 15 - 624 | AA428452, AA134294, T83462, AI219740, AA010048, AI478566, AI990289, AC021747, AL359882, and AC046143. |
| HNBUT01 | 369 | 913838 | 1 - 1090 | 15 - 1104 | AI219740, AI478566, AI632246, AA279757, AA977612, AA716656, AA687260, AI801069, AA071046, AI985849, AW370598, AA630617, AW370599, AW370625, AA134295, AW390691, AI990289, AA134294, AA428452, AI143764, D30955, AW370620, AA352142, AA074442, T83462, AW071043, T79236, and AI744728. |
| HEOQN14 | 370 | 923752 | 1 - 1031 | 15 - 1045 | AI014538, AW006457, AI479414, AI805243, AI290929, AI129301, AI872459, AI601146, AI708870, AI973043, AI540074, AI186894, AI682389, AI654747, AA460832, AI392777, AA405714, AA649837, AI356090, AI358510, AW294364, AA954900, AA991687, AI540589, AI953865, AA977875, AW190678, R61326, R54477, AW009738, AA724308, AW297100, R54409, AA627570, AA504833, AA489470, H08185, R08582, AA778454, AI810108, Z41744, R43473, AA765208, AI698394, Z39824, H19140, Z41120, F03843, AA701889, AA159318, AW408231, AA404221, H84256, AW131981, AI401170, AA405779, AI475002, F01761, AW189730, H84262, F04422, AA404687, AA502309, AA371650, H29188, AA581151, AA477301, AA749407, AA477302, and AI144326. |
| HTXKL86 | 371 | 928194 | 1 - 767 | 15 - 781 | AI810108, W28953, AA313257, AI401170, AW408231, AA371650, H19139, R54508, H10122, R59784, H08285, F08505, Z43765, AI014538, AA504833, R52605, F08180, AA765208, F05493, AA461135, F07194, R13641, AA701889, AA159318, Z45409, AW407594, H84256, AA404221, R13670, F07185, H84262, AA404687, AW407965, AI144326, AW006457, and AA581151. |
| HDQGV77 | 372 | 937546 | 1 - 1876 | 15 - 1890 | |
| HE8TM80 | 373 | 955022 | 1 - 741 | 15 - 755 | R56714, AA125853, AA127005, H06566, T70821, AA307834, H53723, and AF191018. |
| HWLEY40 | 374 | 957875 | 1 - 1443 | 15 - 1457 | W28953, AI810108, AA159318, AA461135, H10122, AA313257, AA701889, AI654981, AI401170, H19139, H08285, AW408231, AA371650, R54508, R59784, AW407594, F07194, AA504833, F08180, F08505, Z43765, R52605, F07185, H84256, AW407965, F05493, H84262, AA404221, R13670, AA765208, Z45409, AA404687, R13641, AI014538, AI144326, AC006171, AC006171, and AL161645. |
| HDPPD36 | 375 | 493820 | 1 - 546 | 15 - 560 | |
| HOUBZ94 | 376 | 527876 | 1 - 139 | 15 - 153 | AC005954, AC005954, and AC068475. |
| HMIAH32 | 377 | 550977 | 1 - 689 | 15 - 703 | |
| HDPTH43 | 378 | 573418 | 1 - 434 | 15 - 448 | |
| HCE3W04 | 379 | 615501 | 1 - 859 | 15 - 873 | AC025165, AC025165, AC022506, AC022506, and AC022366. |
| HMUBZ20 | 380 | 670393 | 1 - 349 | 15 - 363 | |

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|---------|-----|--------|----------|-----------|---|
| HDPAB51 | 381 | 685665 | 1 - 941 | 15 - 955 | |
| HPJAP28 | 382 | 686349 | 1 - 432 | 15 - 446 | AC004794, AC004794, and AC004794. |
| HIBEC79 | 383 | 703000 | 1 - 325 | 15 - 339 | AC011458, AC011458, and AC011458. |
| HOQBF64 | 384 | 703177 | 1 - 389 | 15 - 403 | |
| HTEDL38 | 385 | 761609 | 1 - 547 | 15 - 561 | |
| HE9HI71 | 386 | 779375 | 1 - 668 | 15 - 682 | |
| HNFHS82 | 387 | 779946 | 1 - 401 | 15 - 415 | AC010835. |
| HOUHO89 | 388 | 786548 | 1 - 895 | 15 - 909 | |
| HFPBB28 | 389 | 844526 | 1 - 321 | 15 - 335 | AC016135, AC002518, AC073717, and AC018512. |
| HHEWQ61 | 390 | 876063 | 1 - 1052 | 15 - 1066 | |
| HUFGH09 | 391 | 877078 | 1 - 635 | 15 - 649 | |
| HLICA79 | 392 | 880881 | 1 - 2031 | 15 - 2045 | |
| HSLIH01 | 393 | 884251 | 1 - 1868 | 15 - 1882 | |
| HE9OV91 | 394 | 887364 | 1 - 774 | 15 - 788 | |
| HHEDS85 | 395 | 894602 | 1 - 491 | 15 - 505 | |
| HNTDJ68 | 396 | 899624 | 1 - 2389 | 15 - 2403 | |
| HKAHO77 | 397 | 906671 | 1 - 699 | 15 - 713 | |
| HTFNP84 | 398 | 909687 | 1 - 2474 | 15 - 2488 | |
| HDQGZ78 | 399 | 909735 | 1 - 428 | 15 - 442 | AC026282. |
| HHEMD52 | 400 | 909742 | 1 - 1605 | 15 - 1619 | |
| HSIDQ38 | 401 | 909854 | 1 - 783 | 15 - 797 | AC003070. |
| HSKBF02 | 402 | 909855 | 1 - 383 | 15 - 397 | |
| HIBDE74 | 403 | 766011 | 1 - 508 | 15 - 522 | |
| HWMAE53 | 404 | 909877 | 1 - 436 | 15 - 450 | |
| HFXCG28 | 405 | 909961 | 1 - 596 | 15 - 610 | |
| HFTCU45 | 406 | 910053 | 1 - 538 | 15 - 552 | |
| HFTBL33 | 407 | 910055 | 1 - 1475 | 15 - 1489 | AC025165, AC025165, and AC022366. |
| HTXJA84 | 408 | 911387 | 1 - 900 | 15 - 914 | |
| HKAAW89 | 409 | 911389 | 1 - 433 | 15 - 447 | |
| HSXDD55 | 410 | 911460 | 1 - 1164 | 15 - 1178 | |
| HUFCI64 | 411 | 911558 | 1 - 759 | 15 - 773 | AC004151, and AC004151. |
| HWAF784 | 412 | 911559 | 1 - 1342 | 15 - 1356 | AC004151, and AC004151. |
| HETCL18 | 413 | 914535 | 1 - 1388 | 15 - 1402 | |
| HCRNK75 | 414 | 914536 | 1 - 2256 | 15 - 2270 | |
| HTPFA03 | 415 | 922765 | 1 - 315 | 15 - 329 | |
| HWADR60 | 416 | 926487 | 1 - 1275 | 15 - 1289 | AC023176, and AC023176. |
| HWLFJ01 | 417 | 928017 | 1 - 781 | 15 - 795 | |
| HTXNG95 | 418 | 928577 | 1 - 1380 | 15 - 1394 | |
| HPCIG66 | 419 | 930886 | 1 - 945 | 15 - 959 | AC024888, AC024888, and AC024888. |
| HCRPU72 | 420 | 931140 | 1 - 931 | 15 - 945 | AC023151. |
| HE9RT95 | 421 | 934556 | 1 - 804 | 15 - 818 | AC022420, AC022420, AC022420, and AC008439. |
| HFXJM13 | 422 | 935725 | 1 - 426 | 15 - 440 | |
| HDPWU37 | 423 | 940705 | 1 - 522 | 15 - 536 | |
| HHSDL85 | 424 | 942246 | 1 - 760 | 15 - 774 | |
| HTJMD31 | 425 | 942848 | 1 - 638 | 15 - 652 | |
| HWADD57 | 426 | 943039 | 1 - 996 | 15 - 1010 | AC011492, and AC011492. |
| HLWAH05 | 427 | 944904 | 1 - 1338 | 15 - 1352 | |
| HDPCI84 | 428 | 945527 | 1 - 2479 | 15 - 2493 | |
| HBXDJ07 | 429 | 946830 | 1 - 1470 | 15 - 1484 | H11405, R55569, N27906, H20863, N25140, and U27708. |
| HAMFD12 | 430 | 952438 | 1 - 526 | 15 - 540 | |
| HFKHR40 | 431 | 952470 | 1 - 2240 | 15 - 2254 | AC061707, AC061707, AC061707, AC018805, and AC018805. |
| HDTAI08 | 432 | 953265 | 1 - 590 | 15 - 604 | |
| HMKCX80 | 433 | 956254 | 1 - 1174 | 15 - 1188 | |

TABLE 4

| Code | Description | Tissue | Organ | Cell Line | Disease | Vector |
|-------|-----------------------------|-----------------------------|-------|-----------|---------|--------|
| AR022 | a_Heart | a_Heart | | | | |
| AR023 | a_Liver | a_Liver | | | | |
| AR024 | a_mammary gland | a_mammary gland | | | | |
| AR025 | a_Prostate | a_Prostate | | | | |
| AR026 | a_small intestine | a_small intestine | | | | |
| AR027 | a_Stomach | a_Stomach | | | | |
| AR028 | Blood B cells | Blood B cells | | | | |
| AR029 | Blood B cells activated | Blood B cells activated | | | | |
| AR030 | Blood B cells resting | Blood B cells resting | | | | |
| AR031 | Blood T cells activated | Blood T cells activated | | | | |
| AR032 | Blood T cells resting | Blood T cells resting | | | | |
| AR033 | brain | brain | | | | |
| AR034 | breast | breast | | | | |
| AR035 | breast cancer | breast cancer | | | | |
| AR036 | Cell Line CAOV3 | Cell Line CAOV3 | | | | |
| AR037 | cell line PA-1 | cell line PA-1 | | | | |
| AR038 | cell line transformed | cell line transformed | | | | |
| AR039 | colon | colon | | | | |
| AR040 | colon (9808co65R) | colon (9808co65R) | | | | |
| AR041 | colon (9809co15) | colon (9809co15) | | | | |
| AR042 | colon cancer | colon cancer | | | | |
| AR043 | colon cancer (9808co64R) | colon cancer (9808co64R) | | | | |
| AR044 | colon cancer 9809co14 | colon cancer 9809co14 | | | | |
| AR045 | corn clone 5 | corn clone 5 | | | | |
| AR046 | corn clone 6 | corn clone 6 | | | | |
| AR047 | corn clone2 | corn clone2 | | | | |
| AR048 | corn clone3 | corn clone3 | | | | |
| AR049 | Corn Clone4 | Corn Clone4 | | | | |
| AR050 | Donor II B Cells 24hrs | Donor II B Cells 24hrs | | | | |
| AR051 | Donor II B Cells 72hrs | Donor II B Cells 72hrs | | | | |
| AR052 | Donor II B-Cells 24 hrs. | Donor II B-Cells 24 hrs. | | | | |
| AR053 | Donor II B-Cells 72hrs | Donor II B-Cells 72hrs | | | | |
| AR054 | Donor II Resting B Cells | Donor II Resting B Cells | | | | |
| AR055 | Heart | Heart | | | | |
| AR056 | Human Lung (clonotech) | Human Lung (clonotech) | | | | |
| AR057 | Human Mammary (clontech) | Human Mammary (clontech) | | | | |

| | | | | | | |
|-------|--|---|--|--|--|--|
| AR058 | Human Thymus (clonotech) | Human Thymus (clonotech) | | | | |
| AR059 | Jurkat (unstimulated) | Jurkat (unstimulated) | | | | |
| AR060 | Kidney | Kidney | | | | |
| AR061 | Liver | Liver | | | | |
| AR062 | Liver (Clontech) | Liver (Clontech) | | | | |
| AR063 | Lymphocytes chronic lymphocytic leukaemia | Lymphocytes chronic lymphocytic leukaemia | | | | |
| AR064 | Lymphocytes diffuse large B cell lymphoma | Lymphocytes diffuse large B cell lymphoma | | | | |
| AR065 | Lymphocytes follicular lymphoma | Lymphocytes follicular lymphoma | | | | |
| AR066 | normal breast | normal breast | | | | |
| AR067 | Normal Ovarian (4004901) | Normal Ovarian (4004901) | | | | |
| AR068 | Normal Ovary 9508G045 | Normal Ovary 9508G045 | | | | |
| AR069 | Normal Ovary 9701G208 | Normal Ovary 9701G208 | | | | |
| AR070 | Normal Ovary 9806G005 | Normal Ovary 9806G005 | | | | |
| AR071 | Ovarian Cancer | Ovarian Cancer | | | | |
| AR072 | Ovarian Cancer (9702G001) | Ovarian Cancer (9702G001) | | | | |
| AR073 | Ovarian Cancer (9707G029) | Ovarian Cancer (9707G029) | | | | |
| AR074 | Ovarian Cancer (9804G011) | Ovarian Cancer (9804G011) | | | | |
| AR075 | Ovarian Cancer (9806G019) | Ovarian Cancer (9806G019) | | | | |
| AR076 | Ovarian Cancer (9807G017) | Ovarian Cancer (9807G017) | | | | |
| AR077 | Ovarian Cancer (9809G001) | Ovarian Cancer (9809G001) | | | | |
| AR078 | ovarian cancer 15799 | ovarian cancer 15799 | | | | |
| AR079 | Ovarian Cancer 17717AID | Ovarian Cancer 17717AID | | | | |
| AR080 | Ovarian Cancer 4004664B1 | Ovarian Cancer 4004664B1 | | | | |
| AR081 | Ovarian Cancer 4005315A1 | Ovarian Cancer 4005315A1 | | | | |
| AR082 | ovarian cancer 94127303 | ovarian cancer 94127303 | | | | |
| AR083 | Ovarian Cancer 96069304 | Ovarian Cancer 96069304 | | | | |
| AR084 | Ovarian Cancer 9707G029 | Ovarian Cancer 9707G029 | | | | |
| AR085 | Ovarian Cancer 9807G045 | Ovarian Cancer 9807G045 | | | | |

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|-------|------------------------------------|------------------------------------|--------------|--|--|---------------|
| AR086 | ovarian cancer 9809G001 | ovarian cancer 9809G001 | | | | |
| AR087 | Ovarian Cancer 9905C032RC | Ovarian Cancer 9905C032RC | | | | |
| AR088 | Ovarian cancer 9907 C00 3rd | Ovarian cancer 9907 C00 3rd | | | | |
| AR089 | Prostate | Prostate | | | | |
| AR090 | Prostate (clonotech) | Prostate (clonotech) | | | | |
| AR091 | prostate cancer | prostate cancer | | | | |
| AR092 | prostate cancer #15176 | prostate cancer #15176 | | | | |
| AR093 | prostate cancer #15509 | prostate cancer #15509 | | | | |
| AR094 | prostate cancer #15673 | prostate cancer #15673 | | | | |
| AR095 | Small Intestine (Clontech) | Small Intestine (Clontech) | | | | |
| AR096 | Spleen | Spleen | | | | |
| AR097 | Thymus T cells activated | Thymus T cells activated | | | | |
| AR098 | Thymus T cells resting | Thymus T cells resting | | | | |
| AR099 | Tonsil | Tonsil | | | | |
| AR100 | Tonsil germinal center centroblast | Tonsil germinal center centroblast | | | | |
| AR101 | Tonsil germinal center B cell | Tonsil germinal center B cell | | | | |
| AR102 | Tonsil lymph node | Tonsil lymph node | | | | |
| AR103 | Tonsil memory B cell | Tonsil memory B cell | | | | |
| AR104 | Whole Brain | Whole Brain | | | | |
| AR105 | Xenograft ES-2 | Xenograft ES-2 | | | | |
| AR106 | Xenograft SW626 | Xenograft SW626 | | | | |
| H0002 | Human Adult Heart | Human Adult Heart | Heart | | | Uni-ZAP XR |
| H0004 | Human Adult Spleen | Human Adult Spleen | Spleen | | | Uni-ZAP XR |
| H0008 | Whole 6 Week Old Embryo | | | | | Uni-ZAP XR |
| H0009 | Human Fetal Brain | | | | | Uni-ZAP XR |
| H0011 | Human Fetal Kidney | Human Fetal Kidney | Kidney | | | Uni-ZAP XR |
| H0012 | Human Fetal Kidney | Human Fetal Kidney | Kidney | | | Uni-ZAP XR |
| H0013 | Human 8 Week Whole Embryo | Human 8 Week Old Embryo | Embryo | | | Uni-ZAP XR |
| H0014 | Human Gall Bladder | Human Gall Bladder | Gall Bladder | | | Uni-ZAP XR |
| H0015 | Human Gall Bladder, fraction II | Human Gall Bladder | Gall Bladder | | | Uni-ZAP XR |
| H0022 | Jurkat Cells | Jurkat T-Cell Line | | | | Lambda ZAP II |
| H0023 | Human Fetal Lung | | | | | Uni-ZAP XR |
| H0024 | Human Fetal Lung III | Human Fetal Lung | Lung | | | Uni-ZAP XR |
| H0025 | Human Adult Lymph Node | Human Adult Lymph Node | Lymph Node | | | Lambda ZAP II |
| H0026 | Namalwa Cells | Namalwa B-Cell | | | | Lambda ZAP II |

| | | Line, EBV immortalized | | | | |
|-------|---|--|-------------------|-----------|---------|---------------|
| H0027 | Human Ovarian Cancer | | | | disease | Uni-ZAP XR |
| H0028 | Human Old Ovary | Human Old Ovary | Ovary | | | pBluescript |
| H0029 | Human Pancreas | Human Pancreas | Pancreas | | | Uni-ZAP XR |
| H0030 | Human Placenta | | | | | Uni-ZAP XR |
| H0031 | Human Placenta | Human Placenta | Placenta | | | Uni-ZAP XR |
| H0032 | Human Prostate | Human Prostate | Prostate | | | Uni-ZAP XR |
| H0033 | Human Pituitary | Human Pituitary | | | | Uni-ZAP XR |
| H0036 | Human Adult Small Intestine | Human Adult Small Intestine | Small Int. | | | Uni-ZAP XR |
| H0037 | Human Adult Small Intestine | Human Adult Small Intestine | Small Int. | | | pBluescript |
| H0038 | Human Testes | Human Testes | Testis | | | Uni-ZAP XR |
| H0039 | Human Pancreas Tumor | Human Pancreas Tumor | Pancreas | | disease | Uni-ZAP XR |
| H0040 | Human Testes Tumor | Human Testes Tumor | Testis | | disease | Uni-ZAP XR |
| H0041 | Human Fetal Bone | Human Fetal Bone | Bone | | | Uni-ZAP XR |
| H0042 | Human Adult Pulmonary | Human Adult Pulmonary | Lung | | | Uni-ZAP XR |
| H0046 | Human Endometrial Tumor | Human Endometrial Tumor | Uterus | | disease | Uni-ZAP XR |
| H0050 | Human Fetal Heart | Human Fetal Heart | Heart | | | Uni-ZAP XR |
| H0051 | Human Hippocampus | Human Hippocampus | Brain | | | Uni-ZAP XR |
| H0052 | Human Cerebellum | Human Cerebellum | Brain | | | Uni-ZAP XR |
| H0056 | Human Umbilical Vein, Endo. remake | Human Umbilical Vein Endothelial Cells | Umbilical vein | | | Uni-ZAP XR |
| H0057 | Human Fetal Spleen | | | | | Uni-ZAP XR |
| H0059 | Human Uterine Cancer | Human Uterine Cancer | Uterus | | disease | Lambda ZAP II |
| H0063 | Human Thymus | Human Thymus | Thymus | | | Uni-ZAP XR |
| H0064 | Human Right Hemisphere of Brain | Human Brain, right hemisphere | Brain | | | Uni-ZAP XR |
| H0068 | Human Skin Tumor | Human Skin Tumor | Skin | | disease | Uni-ZAP XR |
| H0069 | Human Activated T-Cells | Activated T-Cells | Blood | Cell Line | | Uni-ZAP XR |
| H0071 | Human Infant Adrenal Gland | Human Infant Adrenal Gland | Adrenal gland | | | Uni-ZAP XR |
| H0075 | Human Activated T-Cells (II) | Activated T-Cells | Blood | Cell Line | | Uni-ZAP XR |
| H0079 | Human Whole 7 Week Old Embryo (II) | Human Whole 7 Week Old Embryo | Embryo | | | Uni-ZAP XR |
| H0081 | Human Fetal Epithelium (Skin) | Human Fetal Skin | Skin | | | Uni-ZAP XR |
| H0082 | Human Fetal Muscle | Human Fetal Muscle | Sk Muscle | | | Uni-ZAP XR |
| H0083 | HUMAN JURKAT MEMBRANE BOUND POLYSOMES | Jurkat Cells | | | | Uni-ZAP XR |
| H0085 | Human Colon | Human Colon | | | | Lambda ZAP II |
| H0086 | Human epithelioid | Epithelioid | Sk Muscle | | disease | Uni-ZAP XR |

| | | | | | | |
|-------|--|---|---------------|-----------|---------|---------------|
| | sarcoma | Sarcoma, muscle | | | | |
| H0087 | Human Thymus | Human Thymus | | | | pBluescript |
| H0090 | Human T-Cell Lymphoma | T-Cell Lymphoma | T-Cell | | disease | Uni-ZAP XR |
| H0092 | Human Pancreas Tumor | Human Pancreas Tumor | Pancreas | | disease | Uni-ZAP XR |
| H0098 | Human Adult Liver, subtracted | Human Adult Liver | Liver | | | Uni-ZAP XR |
| H0100 | Human Whole Six Week Old Embryo | Human Whole Six Week Old Embryo | Embryo | | | Uni-ZAP XR |
| H0101 | Human 7 Weeks Old Embryo, subtracted | Human Whole 7 Week Old Embryo | Embryo | | | Lambda ZAP II |
| H0102 | Human Whole 6 Week Old Embryo (II), subt | Human Whole Six Week Old Embryo | Embryo | | | pBluescript |
| H0105 | Human Fetal Heart, subtracted | Human Fetal Heart | Heart | | | pBluescript |
| H0107 | Human Infant Adrenal Gland, subtracted | Human Infant Adrenal Gland | Adrenal gland | | | pBluescript |
| H0108 | Human Adult Lymph Node, subtracted | Human Adult Lymph Node | Lymph Node | | | Uni-ZAP XR |
| H0111 | Human Placenta, subtracted | Human Placenta | Placenta | | | pBluescript |
| H0112 | Human Parathyroid Tumor, subtracted | Human Parathyroid Tumor | Parathyroid | | | pBluescript |
| H0118 | Human Adult Kidney | Human Adult Kidney | Kidney | | | Uni-ZAP XR |
| H0122 | Human Adult Skeletal Muscle | Human Skeletal Muscle | Sk Muscle | | | Uni-ZAP XR |
| H0123 | Human Fetal Dura Mater | Human Fetal Dura Mater | Brain | | | Uni-ZAP XR |
| H0124 | Human Rhabdomyosarcoma | Human Rhabdomyosarcoma | Sk Muscle | | disease | Uni-ZAP XR |
| H0125 | Cem cells cyclohexamide treated | Cyclohexamide Treated Cem, Jurkat, Raji, and Supt | Blood | Cell Line | | Uni-ZAP XR |
| H0130 | LNCAP untreated | LNCAP Cell Line | Prostate | Cell Line | | Uni-ZAP XR |
| H0131 | LNCAP + 0.3nM R1881 | LNCAP Cell Line | Prostate | Cell Line | | Uni-ZAP XR |
| H0132 | LNCAP + 30nM R1881 | LNCAP Cell Line | Prostate | Cell Line | | Uni-ZAP XR |
| H0134 | Raji Cells, cyclohexamide treated | Cyclohexamide Treated Cem, Jurkat, Raji, and Supt | Blood | Cell Line | | Uni-ZAP XR |
| H0135 | Human Synovial Sarcoma | Human Synovial Sarcoma | Synovium | | | Uni-ZAP XR |
| H0136 | Supt Cells, cyclohexamide treated | Cyclohexamide Treated Cem, Jurkat, Raji, and Supt | Blood | Cell Line | | Uni-ZAP XR |
| H0140 | Activated T-Cells, 8 hrs. | Activated T-Cells | Blood | Cell Line | | Uni-ZAP XR |
| H0144 | Nine Week Old Early Stage Human | 9 Wk Old Early Stage Human | Embryo | | | Uni-ZAP XR |
| H0149 | 7 Week Old Early Stage Human, subtracted | Human Whole 7 Week Old Embryo | Embryo | | | Uni-ZAP XR |
| H0150 | Human Epididymus | Epididymis | Testis | | | Uni-ZAP XR |
| H0152 | Early Stage Human Liver, fract (II) | Human Fetal Liver | Liver | | | Uni-ZAP XR |

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|-------|--|-----------------------------------|---------------|-----------|---------|---------------|
| H0154 | Human Fibrosarcoma | Human Skin Fibrosarcoma | Skin | | disease | Uni-ZAP XR |
| H0156 | Human Adrenal Gland Tumor | Human Adrenal Gland Tumor | Adrenal Gland | | disease | Uni-ZAP XR |
| H0159 | Activated T-Cells, 8 hrs., ligation 2 | Activated T-Cells | Blood | Cell Line | | Uni-ZAP XR |
| H0161 | Activated T-Cells, 24 hrs., ligation 2 | Activated T-Cells | Blood | Cell Line | | Uni-ZAP XR |
| H0163 | Human Synovium | Human Synovium | Synovium | | | Uni-ZAP XR |
| H0165 | Human Prostate Cancer, Stage B2 | Human Prostate Cancer, stage B2 | Prostate | | disease | Uni-ZAP XR |
| H0166 | Human Prostate Cancer, Stage B2 fraction | Human Prostate Cancer, stage B2 | Prostate | | disease | Uni-ZAP XR |
| H0169 | Human Prostate Cancer, Stage C fraction | Human Prostate Cancer, stage C | Prostate | | disease | Uni-ZAP XR |
| H0170 | 12 Week Old Early Stage Human | Twelve Week Old Early Stage Human | Embryo | | | Uni-ZAP XR |
| H0171 | 12 Week Old Early Stage Human, II | Twelve Week Old Early Stage Human | Embryo | | | Uni-ZAP XR |
| H0172 | Human Fetal Brain, random primed | Human Fetal Brain | Brain | | | Lambda ZAP II |
| H0175 | H. Adult Spleen, ziplox | | | | | pSport1 |
| H0177 | CAMA1Ee Cell Line | CAMA1Ee Cell Line | Breast | Cell Line | | Uni-ZAP XR |
| H0178 | Human Fetal Brain | Human Fetal Brain | Brain | | | Uni-ZAP XR |
| H0179 | Human Neutrophil | Human Neutrophil | Blood | Cell Line | | Uni-ZAP XR |
| H0180 | Human Primary Breast Cancer | Human Primary Breast Cancer | Breast | | disease | Uni-ZAP XR |
| H0181 | Human Primary Breast Cancer | Human Primary Breast Cancer | Breast | | disease | Uni-ZAP XR |
| H0182 | Human Primary Breast Cancer | Human Primary Breast Cancer | Breast | | disease | Uni-ZAP XR |
| H0187 | Resting T-Cell | T-Cells | Blood | Cell Line | | Lambda ZAP II |
| H0188 | Human Normal Breast | Human Normal Breast | Breast | | | Uni-ZAP XR |
| H0189 | Human Resting Macrophage | Human Macrophage/Monocytes | Blood | Cell Line | | Uni-ZAP XR |
| H0191 | Human Activated Macrophage (LPS), thiour | Human Macrophage/Monocytes | Blood | Cell Line | | Uni-ZAP XR |
| H0194 | Human Cerebellum, subtracted | Human Cerebellum | Brain | | | pBluescript |
| H0196 | Human Cardiomyopathy, subtracted | Human Cardiomyopathy | Heart | | | Uni-ZAP XR |
| H0197 | Human Fetal Liver, subtracted | Human Fetal Liver | Liver | | | Uni-ZAP XR |
| H0199 | Human Fetal Liver, subtracted, neg clone | Human Fetal Liver | Liver | | | Uni-ZAP XR |
| H0201 | Human Hippocampus, subtracted | Human Hippocampus | Brain | | | pBluescript |
| H0208 | Early Stage Human Lung, subtracted | Human Fetal Lung | Lung | | | pBluescript |

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|-------|---|---|------------|-----------|---------|---------------|
| H0212 | Human Prostate, subtracted | Human Prostate | Prostate | | | pBluescript |
| H0213 | Human Pituitary, subtracted | Human Pituitary | | | | Uni-ZAP XR |
| H0216 | Supt cells, cyclohexamide treated, subtracted | Cyclohexamide Treated Cem, Jurkat, Raji, and Supt | Blood | Cell Line | | pBluescript |
| H0217 | Supt cells, cyclohexamide treated, differentially expressed | Cyclohexamide Treated Cem, Jurkat, Raji, and Supt | Blood | Cell Line | | pBluescript |
| H0222 | Activated T-Cells, 8 hrs, subtracted | Activated T-Cells | Blood | Cell Line | | Uni-ZAP XR |
| H0231 | Human Colon, subtraction | Human Colon | | | | pBluescript |
| H0233 | Human Fetal Heart, Differential (Adult-Specific) | Human Fetal Heart | Heart | | | pBluescript |
| H0234 | human colon cancer, metastatic to liver, differentially expressed | Human Colon Cancer, metasticized to liver | Liver | | | pBluescript |
| H0235 | Human colon cancer, metaticized to liver, subtraction | Human Colon Cancer, metasticized to liver | Liver | | | pBluescript |
| H0239 | Human Kidney Tumor | Human Kidney Tumor | Kidney | | disease | Uni-ZAP XR |
| H0241 | C7MCF7 cell line, estrogen treated, subtraction | C7MCF7 Cell Line, estrogen treated | Breast | Cell Line | | Uni-ZAP XR |
| H0244 | Human 8 Week Whole Embryo, subtracted | Human 8 Week Old Embryo | Embryo | | | Uni-ZAP XR |
| H0246 | Human Fetal Liver-Enzyme subtraction | Human Fetal Liver | Liver | | | Uni-ZAP XR |
| H0247 | Human Membrane Bound Polysomes- Enzyme Subtraction | Human Membrane Bound Polysomes | Blood | Cell Line | | Uni-ZAP XR |
| H0249 | HE7, subtracted by hybridization with E7 cDNA | Human Whole 7 Week Old Embryo | Embryo | | | Uni-ZAP XR |
| H0250 | Human Activated Monocytes | Human Monocytes | | | | Uni-ZAP XR |
| H0251 | Human Chondrosarcoma | Human Chondrosarcoma | Cartilage | | disease | Uni-ZAP XR |
| H0252 | Human Osteosarcoma | Human Osteosarcoma | Bone | | disease | Uni-ZAP XR |
| H0253 | Human adult testis, large inserts | Human Adult Testis | Testis | | | Uni-ZAP XR |
| H0254 | Breast Lymph node cDNA library | Breast Lymph Node | Lymph Node | | | Uni-ZAP XR |
| H0255 | breast lymph node CDNA library | Breast Lymph Node | Lymph Node | | | Lambda ZAP II |
| H0257 | HL-60, PMA 4H | HL-60 Cells, PMA stimulated 4H | Blood | Cell Line | | Uni-ZAP XR |
| H0261 | H. cerebellum, Enzyme subtracted | Human Cerebellum | Brain | | | Uni-ZAP XR |

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|-------|--|---------------------------------------|----------------|-----------|---------|---------------|
| H0263 | human colon cancer | Human Colon Cancer | Colon | | disease | Lambda ZAP II |
| H0264 | human tonsils | Human Tonsil | Tonsil | | | Uni-ZAP XR |
| H0265 | Activated T-Cell (12hs)/Thiouridine labelledEco | T-Cells | Blood | Cell Line | | Uni-ZAP XR |
| H0266 | Human Microvascular Endothelial Cells, fract. A | HMEC | Vein | Cell Line | | Lambda ZAP II |
| H0267 | Human Microvascular Endothelial Cells, fract. B | HMEC | Vein | Cell Line | | Lambda ZAP II |
| H0268 | Human Umbilical Vein Endothelial Cells, fract. A | HUVE Cells | Umbilical vein | Cell Line | | Lambda ZAP II |
| H0269 | Human Umbilical Vein Endothelial Cells, fract. B | HUVE Cells | Umbilical vein | Cell Line | | Lambda ZAP II |
| H0271 | Human Neutrophil, Activated | Human Neutrophil - Activated | Blood | Cell Line | | Uni-ZAP XR |
| H0272 | HUMAN TONSILS, FRACTION 2 | Human Tonsil | Tonsil | | | Uni-ZAP XR |
| H0280 | K562 + PMA (36 hrs) | K562 Cell line | cell line | Cell Line | | ZAP Express |
| H0282 | HBGB's differential consolidation | Human Primary Breast Cancer | Breast | | | Uni-ZAP XR |
| H0284 | Human OB MG63 control fraction I | Human Osteoblastoma MG63 cell line | Bone | Cell Line | | Uni-ZAP XR |
| H0286 | Human OB MG63 treated (10 nM E2) fraction I | Human Osteoblastoma MG63 cell line | Bone | Cell Line | | Uni-ZAP XR |
| H0288 | Human OB HOS control fraction I | Human Osteoblastoma HOS cell line | Bone | Cell Line | | Uni-ZAP XR |
| H0290 | Human OB HOS treated (1 nM E2) fraction I | Human Osteoblastoma HOS cell line | Bone | Cell Line | | Uni-ZAP XR |
| H0292 | Human OB HOS treated (10 nM E2) fraction I | Human Osteoblastoma HOS cell line | Bone | Cell Line | | Uni-ZAP XR |
| H0294 | Amniotic Cells - TNF induced | Amniotic Cells - TNF induced | Placenta | Cell Line | | Uni-ZAP XR |
| H0295 | Amniotic Cells - Primary Culture | Amniotic Cells - Primary Culture | Placenta | Cell Line | | Uni-ZAP XR |
| H0298 | HCB'B's differential consolidation | CAMA1Ee Cell Line | Breast | Cell Line | | Uni-ZAP XR |
| H0299 | HCBA's differential consolidation | CAMA1Ee Cell Line | Breast | Cell Line | | Uni-ZAP XR |
| H0300 | CD34 positive cells (Cord Blood) | CD34 Positive Cells | Cord Blood | | | ZAP Express |
| H0305 | CD34 positive cells (Cord Blood) | CD34 Positive Cells | Cord Blood | | | ZAP Express |
| H0306 | CD34 depleted Buffy Coat (Cord Blood) | CD34 Depleted Buffy Coat (Cord Blood) | Cord Blood | | | ZAP Express |
| H0309 | Human Chronic Synovitis | Synovium, Chronic Synovitis/ | Synovium | | disease | Uni-ZAP XR |

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|-------|----------------------------------|-------------------------------------|--------------|-----------|---------|---------------|
| | | Osteoarthritis | | | | |
| H0310 | human caudate nucleus | Brain | Brain | | | Uni-ZAP XR |
| H0316 | HUMAN STOMACH | Human Stomach | Stomach | | | Uni-ZAP XR |
| H0318 | HUMAN B CELL LYMPHOMA | Human B Cell Lymphoma | Lymph Node | | disease | Uni-ZAP XR |
| H0320 | Human frontal cortex | Human Frontal Cortex | Brain | | | Uni-ZAP XR |
| H0327 | human corpus colosum | Human Corpus Callosum | Brain | | | Uni-ZAP XR |
| H0328 | human ovarian cancer | Ovarian Cancer | Ovary | | disease | Uni-ZAP XR |
| H0329 | Dermatofibrosarcoma Protuberance | Dermatofibrosarcoma Protuberans | Skin | | disease | Uni-ZAP XR |
| H0331 | Hepatocellular Tumor | Hepatocellular Tumor | Liver | | disease | Lambda ZAP II |
| H0333 | Hemangiopericytoma | Hemangiopericytoma | Blood vessel | | disease | Lambda ZAP II |
| H0334 | Kidney cancer | Kidney Cancer | Kidney | | disease | Uni-ZAP XR |
| H0339 | Duodenum | Duodenum | | | | Uni-ZAP XR |
| H0340 | Corpus Callosum | Corpus Collosum-93052 | | | | Uni-ZAP XR |
| H0341 | Bone Marrow Cell Line (RS4;11) | Bone Marrow Cell Line RS4;11 | Bone Marrow | Cell Line | | Uni-ZAP XR |
| H0342 | Lingual Gyrus | Lingual Gyrus | Brain | | | Uni-Zap XR |
| H0343 | stomach cancer (human) | Stomach Cancer - 5383A (human) | | | disease | Uni-ZAP XR |
| H0345 | SKIN | Skin - 4000868H | Skin | | | Uni-ZAP XR |
| H0349 | human adult liver cDNA library | Human Adult Liver | Liver | | | pCMVSPORT 1 |
| H0351 | Glioblastoma | Glioblastoma | Brain | | disease | Uni-ZAP XR |
| H0352 | wilm's tumor | Wilm's Tumor | | | disease | Uni-ZAP XR |
| H0355 | Human Liver | Human Liver, normal Adult | | | | pCMVSPORT 1 |
| H0356 | Human Kidney | Human Kidney | Kidney | | | pCMVSPORT 1 |
| H0359 | KMH2 cell line | KMH2 | | | | ZAP Express |
| H0361 | Human rejected kidney | Human Rejected Kidney | | | disease | pBluescript |
| H0364 | Human Osteoclastoma, excised | Human Osteoclastoma | | | disease | pBluescript |
| H0365 | Osteoclastoma-normalized B | Human Osteoclastoma | | | disease | Uni-ZAP XR |
| H0366 | L428 cell line | L428 | | | | ZAP Express |
| H0369 | H. Atrophic Endometrium | Atrophic Endometrium and myometrium | | | | Uni-ZAP XR |
| H0370 | H. Lymph node breast Cancer | Lymph node with Met. Breast Cancer | | | disease | Uni-ZAP XR |
| H0372 | Human Testes | Human Testes | Testis | | | pCMVSPORT 1 |
| H0373 | Human Heart | Human Adult Heart | Heart | | | pCMVSPORT 1 |
| H0374 | Human Brain | Human Brain | | | | pCMVSPORT 1 |
| H0375 | Human Lung | Human Lung | | | | pCMVSPORT 1 |
| H0376 | Human Spleen | Human Adult Spleen | Spleen | | | pCMVSPORT 1 |

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|-------|--|---------------------------------------|----------------|-----------|---------|---------------|
| H0379 | Human Tongue, frac I | Human Tongue | | | | pSport1 |
| H0381 | Bone Cancer | Bone Cancer | | | disease | Uni-ZAP XR |
| H0383 | Human Prostate BPH, re-excision | Human Prostate BPH | | | | Uni-ZAP XR |
| H0384 | Brain, Kozak | Human Brain | | | | pCMVSPORT 1 |
| H0386 | Leukocyte and Lung; 4 screens | Human Leukocytes | Blood | Cell Line | | pCMVSPORT 1 |
| H0388 | Human Rejected Kidney, 704 re-excision | Human Rejected Kidney | | | disease | pBluescript |
| H0390 | Human Amygdala Depression, re-excision | Human Amygdala Depression | | | disease | pBluescript |
| H0391 | H. Meningioma, M6 | Human Meningioma | brain | | | pSport1 |
| H0392 | H. Meningioma, M1 | Human Meningioma | brain | | | pSport1 |
| H0393 | Fetal Liver, subtraction II | Human Fetal Liver | Liver | | | pBluescript |
| H0394 | A-14 cell line | Redd-Sternberg cell | | | | ZAP Express |
| H0395 | A1-CELL LINE | Redd-Sternberg cell | | | | ZAP Express |
| H0396 | L1 Cell line | Redd-Sternberg cell | | | | ZAP Express |
| H0399 | Human Kidney Cortex, re-rescue | Human Kidney Cortex | | | | Lambda ZAP II |
| H0400 | Human Striatum Depression, re-rescue | Human Brain, Striatum Depression | Brain | | | Lambda ZAP II |
| H0401 | Human Pituitary, subtracted V | Human Pituitary | | | | pBluescript |
| H0402 | CD34 depleted Buffy Coat (Cord Blood), re-excision | CD34 Depleted Buffy Coat (Cord Blood) | Cord Blood | | | ZAP Express |
| H0408 | Human kidney Cortex, subtracted | Human Kidney Cortex | | | | pBluescript |
| H0409 | H. Striatum Depression, subtracted | Human Brain, Striatum Depression | Brain | | | pBluescript |
| H0411 | H Female Bladder, Adult | Human Female Adult Bladder | Bladder | | | pSport1 |
| H0412 | Human umbilical vein endothelial cells, IL-4 induced | HUVE Cells | Umbilical vein | Cell Line | | pSport1 |
| H0413 | Human Umbilical Vein Endothelial Cells, uninduced | HUVE Cells | Umbilical vein | Cell Line | | pSport1 |
| H0414 | Ovarian Tumor I, OV5232 | Ovarian Tumor, OV5232 | Ovary | | disease | pSport1 |
| H0415 | H. Ovarian Tumor, II, OV5232 | Ovarian Tumor, OV5232 | Ovary | | disease | pCMVSPORT 2.0 |
| H0416 | Human Neutrophils, Activated, re-excision | Human Neutrophil - Activated | Blood | Cell Line | | pBluescript |
| H0417 | Human Pituitary, subtracted VIII | Human Pituitary | | | | pBluescript |
| H0421 | Human Bone Marrow, re-excision | Bone Marrow | | | | pBluescript |
| H0422 | T-Cell PHA 16 hrs | T-Cells | Blood | Cell Line | | pSport1 |
| H0423 | T-Cell PHA 24 hrs | T-Cells | Blood | Cell Line | | pSport1 |
| H0424 | Human Pituitary, subt IX | Human Pituitary | | | | pBluescript |
| H0427 | Human Adipose | Human Adipose, left hiplipoma | | | | pSport1 |

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|-------|---|---|----------------|-----------|---------|---------------|
| H0428 | Human Ovary | Human Ovary Tumor | Ovary | | | pSport1 |
| H0429 | K562 + PMA (36 hrs),re-excision | K562 Cell line | cell line | Cell Line | | ZAP Express |
| H0431 | H. Kidney Medulla, re-excision | Kidney medulla | Kidney | | | pBluescript |
| H0433 | Human Umbilical Vein Endothelial cells, frac B, re-excision | HUVE Cells | Umbilical vein | Cell Line | | pBluescript |
| H0434 | Human Brain, striatum, re-excision | Human Brain, Striatum | | | | pBluescript |
| H0435 | Ovarian Tumor 10-3-95 | Ovarian Tumor, OV350721 | Ovary | | | pCMVSport 2.0 |
| H0436 | Resting T-Cell Library,II | T-Cells | Blood | Cell Line | | pSport1 |
| H0437 | H Umbilical Vein Endothelial Cells, frac A, re-excision | HUVE Cells | Umbilical vein | Cell Line | | Lambda ZAP II |
| H0438 | H. Whole Brain #2, re-excision | Human Whole Brain #2 | | | | ZAP Express |
| H0441 | H. Kidney Cortex, subtracted | Kidney cortex | Kidney | | | pBluescript |
| H0443 | H. Adipose, subtracted | Human Adipose, left hiplipoma | | | | pSport1 |
| H0444 | Spleen metastatic melanoma | Spleen, Metastatic malignant melanoma | Spleen | | disease | pSport1 |
| H0445 | Spleen, Chronic lymphocytic leukemia | Human Spleen, CLL | Spleen | | disease | pSport1 |
| H0453 | H. Kidney Pyramid, subtracted | Kidney pyramids | Kidney | | | pBluescript |
| H0455 | H. Striatum Depression, subt | Human Brain, Striatum Depression | Brain | | | pBluescript |
| H0457 | Human Eosinophils | Human Eosinophils | | | | pSport1 |
| H0458 | CD34+ cell, I, frac II | CD34 positive cells | | | | pSport1 |
| H0459 | CD34+cells, II, FRACTION 2 | CD34 positive cells | | | | pCMVSport 2.0 |
| H0462 | H. Amygdala Depression, subtracted | | Brain | | | pBluescript |
| H0477 | Human Tonsil, Lib 3 | Human Tonsil | Tonsil | | | pSport1 |
| H0478 | Salivary Gland, Lib 2 | Human Salivary Gland | Salivary gland | | | pSport1 |
| H0479 | Salivary Gland, Lib 3 | Human Salivary Gland | Salivary gland | | | pSport1 |
| H0483 | Breast Cancer cell line, MDA 36 | Breast Cancer Cell line, MDA 36 | | | | pSport1 |
| H0484 | Breast Cancer Cell line, angiogenic | Breast Cancer Cell line, Angiogenic, 36T3 | | | | pSport1 |
| H0485 | Hodgkin's Lymphoma I | Hodgkin's Lymphoma I | | | disease | pCMVSport 2.0 |
| H0486 | Hodgkin's Lymphoma II | Hodgkin's Lymphoma II | | | disease | pCMVSport 2.0 |
| H0487 | Human Tonsils, lib I | Human Tonsils | | | | pCMVSport 2.0 |

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|-------|---|--|------------|------------|---------|---------------|
| H0488 | Human Tonsils, Lib 2 | Human Tonsils | | | | pCMVSPORT 2.0 |
| H0489 | Crohn's Disease | Ileum | Intestine | | disease | pSport1 |
| H0492 | HL-60, RA 4h, Subtracted | HL-60 Cells, RA stimulated for 4H | Blood | Cell Line | | Uni-ZAP XR |
| H0494 | Keratinocyte | Keratinocyte | | | | pCMVSPORT 2.0 |
| H0497 | HEL cell line | HEL cell line | | HEL 92.1.7 | | pSport1 |
| H0505 | Human Astrocyte | Human Astrocyte | | | | pSport1 |
| H0506 | Ulcerative Colitis | Colon | Colon | | | pSport1 |
| H0509 | Liver, Hepatoma | Human Liver, Hepatoma, patient 8 | Liver | | disease | pCMVSPORT 3.0 |
| H0510 | Human Liver, normal | Human Liver, normal, Patient # 8 | Liver | | | pCMVSPORT 3.0 |
| H0517 | Nasal polyps | Nasal polyps | | | | pCMVSPORT 2.0 |
| H0518 | pBMC stimulated w/ poly I/C | pBMC stimulated with poly I/C | | | | pCMVSPORT 3.0 |
| H0519 | NTERA2, control | NTERA2, Teratocarcinoma cell line | | | | pCMVSPORT 3.0 |
| H0520 | NTERA2 + retinoic acid, 14 days | NTERA2, Teratocarcinoma cell line | | | | pSport1 |
| H0521 | Primary Dendritic Cells, lib 1 | Primary Dendritic cells | | | | pCMVSPORT 3.0 |
| H0522 | Primary Dendritic cells, frac 2 | Primary Dendritic cells | | | | pCMVSPORT 3.0 |
| H0525 | PCR, pBMC I/C treated | pBMC stimulated with poly I/C | | | | PCR11 |
| H0528 | Poly[I]/Poly[C] Normal Lung Fibroblasts | Poly[I]/Poly[C] Normal Lung Fibroblasts | | | | pCMVSPORT 3.0 |
| H0529 | Myeloid Progenitor Cell Line | TF-1 Cell Line; Myeloid progenitor cell line | | | | pCMVSPORT 3.0 |
| H0530 | Human Dermal Endothelial Cells, untreated | Human Dermal Endothelial Cells; untreated | | | | pSport1 |
| H0538 | Merkel Cells | Merkel cells | Lymph node | | | pSport1 |
| H0539 | Pancreas Islet Cell Tumor | Pancreas Islet Cell Tumour | Pancreas | | disease | pSport1 |
| H0540 | Skin, burned | Skin, leg burned | Skin | | | pSport1 |
| H0542 | T Cell helper I | Helper T cell | | | | pCMVSPORT 3.0 |
| H0543 | T cell helper II | Helper T cell | | | | pCMVSPORT 3.0 |
| H0544 | Human endometrial stromal cells | Human endometrial stromal cells | | | | pCMVSPORT 3.0 |
| H0545 | Human endometrial stromal cells-treated with progesterone | Human endometrial stromal cells-treated with proge | | | | pCMVSPORT 3.0 |
| H0546 | Human endometrial stromal cells-treated with estradiol | Human endometrial stromal cells-treated with estra | | | | pCMVSPORT 3.0 |
| H0547 | NTERA2 teratocarcinoma cell line+retinoic acid (14 | NTERA2, Teratocarcinoma | | | | pSport1 |

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|-------|---|---|-------------|-----------|---------|---------------|
| | days) | cell line | | | | |
| H0549 | H. Epididymus, caput & corpus | Human Epididymus, caput and corpus | | | | Uni-ZAP XR |
| H0550 | H. Epididymus, cauda | Human Epididymus, cauda | | | | Uni-ZAP XR |
| H0551 | Human Thymus Stromal Cells | Human Thymus Stromal Cells | | | | pCMVSPORT 3.0 |
| H0553 | Human Placenta | Human Placenta | | | | pCMVSPORT 3.0 |
| H0555 | Rejected Kidney, lib 4 | Human Rejected Kidney | Kidney | | disease | pCMVSPORT 3.0 |
| H0556 | Activated T-cell(12h)/Thiouridine-re-excision | T-Cells | Blood | Cell Line | | Uni-ZAP XR |
| H0559 | HL-60, PMA 4H, re-excision | HL-60 Cells, PMA stimulated 4H | Blood | Cell Line | | Uni-ZAP XR |
| H0560 | KMH2 | KMH2 | | | | pCMVSPORT 3.0 |
| H0561 | L428 | L428 | | | | pCMVSPORT 3.0 |
| H0562 | Human Fetal Brain, normalized c5-11-26 | Human Fetal Brain | | | | pCMVSPORT 2.0 |
| H0563 | Human Fetal Brain, normalized 50021F | Human Fetal Brain | | | | pCMVSPORT 2.0 |
| H0566 | Human Fetal Brain,normalized c50F | Human Fetal Brain | | | | pCMVSPORT 2.0 |
| H0569 | Human Fetal Brain, normalized CO | Human Fetal Brain | | | | pCMVSPORT 2.0 |
| H0571 | Human Fetal Brain, normalized C500HE | Human Fetal Brain | | | | pCMVSPORT 2.0 |
| H0572 | Human Fetal Brain, normalized AC5002 | Human Fetal Brain | | | | pCMVSPORT 2.0 |
| H0574 | Hepatocellular Tumor; re-excision | Hepatocellular Tumor | Liver | | disease | Lambda ZAP II |
| H0575 | Human Adult Pulmonary;re-excision | Human Adult Pulmonary | Lung | | | Uni-ZAP XR |
| H0576 | Resting T-Cell; re-excision | T-Cells | Blood | Cell Line | | Lambda ZAP II |
| H0579 | Pericardium | Pericardium | Heart | | | pSPORT1 |
| H0580 | Dendritic cells, pooled | Pooled dendritic cells | | | | pCMVSPORT 3.0 |
| H0581 | Human Bone Marrow, treated | Human Bone Marrow | Bone Marrow | | | pCMVSPORT 3.0 |
| H0583 | B Cell lymphoma | B Cell Lymphoma | B Cell | | disease | pCMVSPORT 3.0 |
| H0584 | Activated T-cells, 24 hrs,re-excision | Activated T-Cells | Blood | Cell Line | | Uni-ZAP XR |
| H0586 | Healing groin wound, 6.5 hours post incision | healing groin wound, 6.5 hours post incision - 2/ | groin | | disease | pCMVSPORT 3.0 |
| H0587 | Healing groin wound; 7.5 hours post incision | Groin-2/19/97 | groin | | disease | pCMVSPORT 3.0 |
| H0589 | CD34 positive cells (cord blood),re-ex | CD34 Positive Cells | Cord Blood | | | ZAP Express |
| H0590 | Human adult small intestine,re-excision | Human Adult Small Intestine | Small Int. | | | Uni-ZAP XR |

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|-------|---|---|----------|--|---------|---------------|
| H0591 | Human T-cell lymphoma;re-excision | T-Cell Lymphoma | T-Cell | | disease | Uni-ZAP XR |
| H0592 | Healing groin wound - zero hr post-incision (control) | HGS wound healing project; abdomen | | | disease | pCMVSPORT 3.0 |
| H0593 | Olfactory epithelium;nasalcavity | Olfactory epithelium from roof of left nasal cavity | | | | pCMVSPORT 3.0 |
| H0594 | Human Lung Cancer;re-excision | Human Lung Cancer | Lung | | disease | Lambda ZAP II |
| H0595 | Stomach cancer (human);re-excision | Stomach Cancer - 5383A (human) | | | disease | Uni-ZAP XR |
| H0596 | Human Colon Cancer;re-excision | Human Colon Cancer | Colon | | | Lambda ZAP II |
| H0597 | Human Colon; re-excision | Human Colon | | | | Lambda ZAP II |
| H0598 | Human Stomach;re-excision | Human Stomach | Stomach | | | Uni-ZAP XR |
| H0599 | Human Adult Heart;re-excision | Human Adult Heart | Heart | | | Uni-ZAP XR |
| H0600 | Healing Abdomen wound;70&90 min post incision | Abdomen | | | disease | pCMVSPORT 3.0 |
| H0601 | Healing Abdomen Wound;15 days post incision | Abdomen | | | disease | pCMVSPORT 3.0 |
| H0602 | Healing Abdomen Wound;21&29 days post incision | Abdomen | | | disease | pCMVSPORT 3.0 |
| H0604 | Human Pituitary, re-excision | Human Pituitary | | | | pBluescript |
| H0606 | Human Primary Breast Cancer;re-excision | Human Primary Breast Cancer | Breast | | disease | Uni-ZAP XR |
| H0607 | H.Leukocytes, normalized cot 50A3 | H.Leukocytes | | | | pCMVSPORT 1 |
| H0609 | H. Leukocytes, normalized cot > 500A | H.Leukocytes | | | | pCMVSPORT 1 |
| H0610 | H. Leukocytes, normalized cot 5A | H.Leukocytes | | | | pCMVSPORT 1 |
| H0611 | H. Leukocytes, normalized cot 500 B | H.Leukocytes | | | | pCMVSPORT 1 |
| H0613 | H.Leukocytes, normalized cot 5B | H.Leukocytes | | | | pCMVSPORT 1 |
| H0615 | Human Ovarian Cancer Reexcision | Ovarian Cancer | Ovary | | disease | Uni-ZAP XR |
| H0616 | Human Testes, Reexcision | Human Testes | Testis | | | Uni-ZAP XR |
| H0617 | Human Primary Breast Cancer Reexcision | Human Primary Breast Cancer | Breast | | disease | Uni-ZAP XR |
| H0618 | Human Adult Testes, Large Inserts, Reexcision | Human Adult Testis | Testis | | | Uni-ZAP XR |
| H0619 | Fetal Heart | Human Fetal Heart | Heart | | | Uni-ZAP XR |
| H0620 | Human Fetal Kidney; Reexcision | Human Fetal Kidney | Kidney | | | Uni-ZAP XR |
| H0622 | Human Pancreas Tumor; | Human Pancreas | Pancreas | | disease | Uni-ZAP XR |

| | Reexcision | Tumor | | | | |
|-------|--|--|-------------------|-----------|---------|---------------|
| H0623 | Human Umbilical Vein; Reexcision | Human Umbilical Vein Endothelial Cells | Umbilical vein | | | Uni-ZAP XR |
| H0624 | 12 Week Early Stage Human II; Reexcision | Twelve Week Old Early Stage Human | Embryo | | | Uni-ZAP XR |
| H0625 | Ku 812F Basophils Line | Ku 812F Basophils | | | | pSport1 |
| H0626 | Saos2 Cells; Untreated | Saos2 Cell Line; Untreated | | | | pSport1 |
| H0627 | Saos2 Cells; Vitamin D3 Treated | Saos2 Cell Line; Vitamin D3 Treated | | | | pSport1 |
| H0628 | Human Pre-Differentiated Adipocytes | Human Pre- Differentiated Adipocytes | | | | Uni-ZAP XR |
| H0629 | Human Leukocyte, control #2 | Human Normalized leukocyte | | | | pCMVSport 1 |
| H0630 | Human Leukocytes,normalized control #4 | Human Normalized leukocyte | | | | pCMVSport 1 |
| H0631 | Saos2, Dexamethosome Treated | Saos2 Cell Line; Dexamethosome Treated | | | | pSport1 |
| H0632 | Hepatocellular Tumor;re- excision | Hepatocellular Tumor | Liver | | | Lambda ZAP II |
| H0633 | Lung Carcinoma A549 TNFalpha activated | TNFalpha activated A549--Lung Carcinoma | | | disease | pSport1 |
| H0634 | Human Testes Tumor, re- excision | Human Testes Tumor | Testis | | disease | Uni-ZAP XR |
| H0635 | Human Activated T-Cells, re-excision | Activated T-Cells | Blood | Cell Line | | Uni-ZAP XR |
| H0637 | Dendritic Cells From CD34 Cells | Dendritic cells from CD34 cells | | | | pSport1 |
| H0638 | CD40 activated monocyte dendritic cells | CD40 activated monocyte dendritic cells | | | | pSport1 |
| H0641 | LPS activated derived dendritic cells | LPS activated monocyte derived dendritic cells | | | | pSport1 |
| H0642 | Hep G2 Cells, lambda library | Hep G2 Cells | | | | Other |
| H0643 | Hep G2 Cells, PCR library | Hep G2 Cells | | | | Other |
| H0644 | Human Placenta (re- excision) | Human Placenta | Placenta | | | Uni-ZAP XR |
| H0645 | Fetal Heart, re-excision | Human Fetal Heart | Heart | | | Uni-ZAP XR |
| H0646 | Lung, Cancer (400513 A3): Invasive Poorly Differentiated Lung Adenocarcinoma, | Metastatic squamous cell lung carcinoma, poorly di | | | | pSport1 |
| H0647 | Lung, Cancer (4005163 B7): Invasive, Poorly Diff. Adenocarcinoma, Metastatic | Invasive poorly differentiated lung adenocarcinoma | | | disease | pSport1 |

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|-------|---|--|-------------------------|--|---------|---------------|
| H0648 | Ovary, Cancer: (4004562 B6) Papillary Serous Cystic Neoplasm, Low Malignant Pot | Papillary Cstic neoplasm of low malignant potentia | | | disease | pSport1 |
| H0649 | Lung, Normal: (4005313 B1) | Normal Lung | | | | pSport1 |
| H0650 | B-Cells | B-Cells | | | | pCMVSPORT 3.0 |
| H0651 | Ovary, Normal: (9805C040R) | Normal Ovary | | | | pSport1 |
| H0652 | Lung, Normal: (4005313 B1) | Normal Lung | | | | pSport1 |
| H0653 | Stromal Cells | Stromal Cells | | | | pSport1 |
| H0656 | B-cells (unstimulated) | B-cells (unstimulated) | | | | pSport1 |
| H0657 | B-cells (stimulated) | B-cells (stimulated) | | | | pSport1 |
| H0658 | Ovary, Cancer (9809C332): Poorly differentiated adenocarcinoma | 9809C332- Poorly differentiate | Ovary & Fallopian Tubes | | disease | pSport1 |
| H0659 | Ovary, Cancer (15395A1F): Grade II Papillary Carcinoma | Grade II Papillary Carcinoma, Ovary | Ovary | | disease | pSport1 |
| H0660 | Ovary, Cancer: (15799A1F) Poorly differentiated carcinoma | Poorly differentiated carcinoma, ovary | | | disease | pSport1 |
| H0661 | Breast, Cancer: (4004943 A5) | Breast cancer | | | disease | pSport1 |
| H0662 | Breast, Normal: (4005522B2) | Normal Breast - #4005522(B2) | Breast | | | pSport1 |
| H0663 | Breast, Cancer: (4005522 A2) | Breast Cancer - #4005522(A2) | Breast | | disease | pSport1 |
| H0664 | Breast, Cancer: (9806C012R) | Breast Cancer | Breast | | disease | pSport1 |
| H0665 | Stromal cells 3.88 | Stromal cells 3.88 | | | | pSport1 |
| H0666 | Ovary, Cancer: (4004332 A2) | Ovarian Cancer, Sample #4004332A2 | | | disease | pSport1 |
| H0667 | Stromal cells(HBM3.18) | Stromal cell(HBM 3.18) | | | | pSport1 |
| H0668 | stromal cell clone 2.5 | stromal cell clone 2.5 | | | | pSport1 |
| H0669 | Breast, Cancer: (4005385 A2) | Breast Cancer (4005385A2) | Breast | | | pSport1 |
| H0670 | Ovary, Cancer(4004650 A3): Well-Differentiated Micropapillary Serous Carcinoma | Ovarian Cancer - 4004650A3 | | | | pSport1 |
| H0671 | Breast, Cancer: (9802C02OE) | Breast Cancer- Sample # 9802C02OE | | | | pSport1 |
| H0672 | Ovary, Cancer: (4004576 A8) | Ovarian Cancer(4004576A8) | Ovary | | | pSport1 |
| H0673 | Human Prostate Cancer, | Human Prostate | Prostate | | | Uni-ZAP XR |

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|-------|---|---|----------|-----------|---------|---------------|
| | Stage B2; re-excision | Cancer, stage B2 | | | | |
| H0674 | Human Prostate Cancer, Stage C; re-excision | Human Prostate Cancer, stage C | Prostate | | | Uni-ZAP XR |
| H0675 | Colon, Cancer: (9808C064R) | Colon Cancer 9808C064R | | | | pCMVSPORT 3.0 |
| H0676 | Colon, Cancer: (9808C064R)-total RNA | Colon Cancer 9808C064R | | | | pCMVSPORT 3.0 |
| H0677 | TNFR degenerate oligo | B-Cells | | | | PCR II |
| H0682 | Serous Papillary Adenocarcinoma | serous papillary adenocarcinoma (9606G304SPA3B) | | | | pCMVSPORT 3.0 |
| H0683 | Ovarian Serous Papillary Adenocarcinoma | Serous papillary adenocarcinoma, stage 3C (9804G01) | | | | pCMVSPORT 3.0 |
| H0684 | Serous Papillary Adenocarcinoma | Ovarian Cancer- 9810G606 | Ovaries | | | pCMVSPORT 3.0 |
| H0685 | Adenocarcinoma of Ovary, Human Cell Line, # OVCAR-3 | Adenocarcinoma of Ovary, Human Cell Line, # OVCAR- | | | | pCMVSPORT 3.0 |
| H0686 | Adenocarcinoma of Ovary, Human Cell Line | Adenocarcinoma of Ovary, Human Cell Line, # SW-626 | | | | pCMVSPORT 3.0 |
| H0687 | Human normal ovary(#9610G215) | Human normal ovary(#9610G215) | Ovary | | | pCMVSPORT 3.0 |
| H0688 | Human Ovarian Cancer(#9807G017) | Human Ovarian cancer(#9807G017), mRNA from Maura Ru | | | | pCMVSPORT 3.0 |
| H0689 | Ovarian Cancer | Ovarian Cancer, #9806G019 | | | | pCMVSPORT 3.0 |
| H0690 | Ovarian Cancer, # 9702G001 | Ovarian Cancer, #9702G001 | | | | pCMVSPORT 3.0 |
| H0691 | Normal Ovary, #9710G208 | normal ovary, #9710G208 | | | | pCMVSPORT 3.0 |
| H0693 | Normal Prostate #ODQ3958EN | Normal Prostate Tissue # ODQ3958EN | | | | pCMVSPORT 3.0 |
| H0695 | mononucleocytes from patient | mononucleocytes from patient at Shady Grove Hospit | | | | pCMVSPORT 3.0 |
| N0006 | Human Fetal Brain | Human Fetal Brain | | | | |
| N0007 | Human Hippocampus | Human Hippocampus | | | | |
| N0009 | Human Hippocampus, prescreened | Human Hippocampus | | | | |
| S0001 | Brain frontal cortex | Brain frontal cortex | Brain | | | Lambda ZAP II |
| S0002 | Monocyte activated | Monocyte-activated | blood | Cell Line | | Uni-ZAP XR |
| S0003 | Human Osteoclastoma | Osteoclastoma | bone | | disease | Uni-ZAP XR |
| S0004 | Prostate | Prostate BPH | Prostate | | | Lambda ZAP II |
| S0005 | Heart | Heart-left ventricle | Heart | | | pCDNA |
| S0007 | Early Stage Human Brain | Human Fetal Brain | | | | Uni-ZAP XR |
| S0010 | Human Amygdala | Amygdala | | | | Uni-ZAP XR |
| S0011 | STROMAL - | Osteoclastoma | bone | | disease | Uni-ZAP XR |

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|-------|---|-------------------------------------|-----------------------|-----------|---------|-------------|
| | OSTEOCLASTOMA | | | | | |
| S0013 | Prostate | Prostate | prostate | | | Uni-ZAP XR |
| S0016 | Kidney Pyramids | Kidney pyramids | Kidney | | | Uni-ZAP XR |
| S0022 | Human Osteoclastoma Stromal Cells - unamplified | Osteoclastoma Stromal Cells | | | | Uni-ZAP XR |
| S0026 | Stromal cell TF274 | stromal cell | Bone marrow | Cell Line | | Uni-ZAP XR |
| S0027 | Smooth muscle, serum treated | Smooth muscle | Pulmonary artery | Cell Line | | Uni-ZAP XR |
| S0028 | Smooth muscle, control | Smooth muscle | Pulmonary artery | Cell Line | | Uni-ZAP XR |
| S0029 | brain stem | Brain stem | brain | | | Uni-ZAP XR |
| S0030 | Brain pons | Brain Pons | Brain | | | Uni-ZAP XR |
| S0031 | Spinal cord | Spinal cord | spinal cord | | | Uni-ZAP XR |
| S0032 | Smooth muscle-ILb induced | Smooth muscle | Pulmonary artery | Cell Line | | Uni-ZAP XR |
| S0036 | Human Substantia Nigra | Human Substantia Nigra | | | | Uni-ZAP XR |
| S0037 | Smooth muscle, IL1b induced | Smooth muscle | Pulmonary artery | Cell Line | | Uni-ZAP XR |
| S0038 | Human Whole Brain #2 - Oligo dT > 1.5Kb | Human Whole Brain #2 | | | | ZAP Express |
| S0040 | Adipocytes | Human Adipocytes from Osteoclastoma | | | | Uni-ZAP XR |
| S0042 | Testes | Human Testes | | | | ZAP Express |
| S0044 | Prostate BPH | prostate BPH | Prostate | | disease | Uni-ZAP XR |
| S0045 | Endothelial cells-control | Endothelial cell | endothelial cell-lung | Cell Line | | Uni-ZAP XR |
| S0046 | Endothelial-induced | Endothelial cell | endothelial cell-lung | Cell Line | | Uni-ZAP XR |
| S0048 | Human Hypothalamus, Alzheimer's | Human Hypothalamus, Alzheimer's | | | disease | Uni-ZAP XR |
| S0049 | Human Brain, Striatum | Human Brain, Striatum | | | | Uni-ZAP XR |
| S0050 | Human Frontal Cortex, Schizophrenia | Human Frontal Cortex, Schizophrenia | | | disease | Uni-ZAP XR |
| S0051 | Human Hypothalamus, Schizophrenia | Human Hypothalamus, Schizophrenia | | | disease | Uni-ZAP XR |
| S0052 | neutrophils control | human neutrophils | blood | Cell Line | | Uni-ZAP XR |
| S0053 | Neutrophils IL-1 and LPS induced | human neutrophil induced | blood | Cell Line | | Uni-ZAP XR |
| S0106 | STRIATUM DEPRESSION | | BRAIN | | disease | Uni-ZAP XR |
| S0112 | Hypothalamus | | Brain | | | Uni-ZAP XR |
| S0114 | Anergic T-cell | Anergic T-cell | | Cell Line | | Uni-ZAP XR |
| S0116 | Bone marrow | Bone marrow | Bone marrow | | | Uni-ZAP XR |
| S0122 | Osteoclastoma-normalized A | Osteoclastoma | bone | | disease | pBluescript |
| S0126 | Osteoblasts | Osteoblasts | Knee | Cell Line | | Uni-ZAP XR |

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|-------|---|---------------------------------------|------------------|-----------|---------|---------------|
| S0132 | Epithelial-TNF α and INF induced | Airway Epithelial | | | | Uni-ZAP XR |
| S0134 | Apoptotic T-cell | apoptotic cells | | Cell Line | | Uni-ZAP XR |
| S0136 | PERM TF274 | stromal cell | Bone marrow | Cell Line | | Lambda ZAP II |
| S0140 | eosinophil-IL5 induced | eosinophil | lung | Cell Line | | Uni-ZAP XR |
| S0142 | Macrophage-oxLDL | macrophage-oxidized LDL treated | blood | Cell Line | | Uni-ZAP XR |
| S0144 | Macrophage (GM-CSF treated) | Macrophage (GM-CSF treated) | | | | Uni-ZAP XR |
| S0146 | prostate-edited | prostate BPH | Prostate | | | Uni-ZAP XR |
| S0148 | Normal Prostate | Prostate | prostate | | | Uni-ZAP XR |
| S0150 | LNCAP prostate cell line | LNCAP Cell Line | Prostate | Cell Line | | Uni-ZAP XR |
| S0152 | PC3 Prostate cell line | PC3 prostate cell line | | | | Uni-ZAP XR |
| S0180 | Bone Marrow Stroma, TNF&LPS ind | Bone Marrow Stroma, TNF & LPS induced | | | disease | Uni-ZAP XR |
| S0182 | Human B Cell 8866 | Human B- Cell 8866 | | | | Uni-ZAP XR |
| S0188 | Prostate,BPH, Lib 2 | Human Prostate BPH | | | disease | pSport1 |
| S0192 | Synovial Fibroblasts (control) | Synovial Fibroblasts | | | | pSport1 |
| S0194 | Synovial hypoxia | Synovial Fibroblasts | | | | pSport1 |
| S0196 | Synovial IL-1/TNF stimulated | Synovial Fibroblasts | | | | pSport1 |
| S0202 | 7TM-pbdd | PBLS, 7TM receptor enriched | | | | PCRII |
| S0206 | Smooth Muscle- HASTE normalized | Smooth muscle | Pulmonary artery | Cell Line | | pBluescript |
| S0208 | Mesangial cell, frac 1 | Mesangial cell | | | | pSport1 |
| S0210 | Mesangial cell, frac 2 | Mesangial cell | | | | pSport1 |
| S0212 | Bone Marrow Stromal Cell, untreated | Bone Marrow Stromal Cell, untreated | | | | pSport1 |
| S0214 | Human Osteoclastoma, re-excision | Osteoclastoma | bone | | disease | Uni-ZAP XR |
| S0216 | Neutrophils IL-1 and LPS induced | human neutrophil induced | blood | Cell Line | | Uni-ZAP XR |
| S0218 | Apoptotic T-cell, re-excision | apoptotic cells | | Cell Line | | Uni-ZAP XR |
| S0220 | H. hypothalamus, frac A;re-excision | Hypothalamus | Brain | | | ZAP Express |
| S0222 | H. Frontal cortex,epileptic;re-excision | H. Brain, Frontal Cortex, Epileptic | Brain | | disease | Uni-ZAP XR |
| S0242 | Synovial Fibroblasts (II1/TNF), subt | Synovial Fibroblasts | | | | pSport1 |
| S0250 | Human Osteoblasts II | Human Osteoblasts | Femur | | disease | pCMVSPORT 2.0 |
| S0252 | 7TM-PIMIX | PBLS, 7TM receptor enriched | | | | PCRII |
| S0260 | Spinal Cord, re-excision | Spinal cord | spinal cord | | | Uni-ZAP XR |
| S0268 | PRMIX | PRMIX (Human | prostate | | | PCRII |

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|-------|---|-------------------------------------|-------------------|-----------|---------|---------------|
| | | Prostate) | | | | |
| S0270 | PTMIX | PTMIX (Human Thymus) | Thymus | | | PCRII |
| S0274 | PCMIX | PCMIX (Human Cerebellum) | Brain | | | PCRII |
| S0276 | Synovial hypoxia-RSF subtracted | Synovial fobroblasts (rheumatoid) | Synovial tissue | | | pSport1 |
| S0278 | H Macrophage (GM-CSF treated), re-excision | Macrophage (GM-CSF treated) | | | | Uni-ZAP XR |
| S0280 | Human Adipose Tissue, re-excision | Human Adipose Tissue | | | | Uni-ZAP XR |
| S0282 | Brain Frontal Cortex, re-excision | Brain frontal cortex | Brain | | | Lambda ZAP II |
| S0294 | Larynx tumor | Larynx tumor | Larynx,vocal cord | | disease | pSport1 |
| S0298 | Bone marrow stroma,treated | Bone marrow stroma,treatedSB | Bone marrow | | | pSport1 |
| S0300 | Frontal lobe,dementia;re-excision | Frontal Lobe dementia/Alzheimer' 's | Brain | | | Uni-ZAP XR |
| S0306 | Larynx normal #10 261-273 | Larynx normal | | | | pSport1 |
| S0310 | Normal trachea | Normal trachea | | | | pSport1 |
| S0312 | Human osteoarthritic;fraction II | Human osteoarthritic cartilage | | | disease | pSport1 |
| S0314 | Human osteoarthritis;fraction I | Human osteoarthritic cartilage | | | disease | pSport1 |
| S0316 | Human Normal Cartilage,Fraction I | Human Normal Cartilage | | | | pSport1 |
| S0318 | Human Normal Cartilage Fraction II | Human Normal Cartilage | | | | pSport1 |
| S0322 | Siebben Polyposis | Siebben Polyposis | | | | pSport1 |
| S0328 | Palate carcinoma | Palate carcinoma | Uvula | | disease | pSport1 |
| S0330 | Palate normal | Palate normal | Uvula | | | pSport1 |
| S0332 | Pharynx carcinoma | Pharynx carcinoma | Hypopharynx | | | pSport1 |
| S0334 | Human Normal Cartilage Fraction III | Human Normal Cartilage | | | | pSport1 |
| S0336 | Human Normal Cartilage Fraction IV | Human Normal Cartilage | | | | pSport1 |
| S0338 | Human Osteoarthritic Cartilage Fraction III | Human osteoarthritic cartilage | | | disease | pSport1 |
| S0340 | Human Osteoarthritic Cartilage Fraction IV | Human osteoarthritic cartilage | | | disease | pSport1 |
| S0342 | Adipocytes;re-excision | Human Adipocytes from Osteoclastoma | | | | Uni-ZAP XR |
| S0344 | Macrophage-oxLDL; re-excision | macrophage-oxidized LDL treated | blood | Cell Line | | Uni-ZAP XR |
| S0346 | Human Amygdala;re- | Amygdala | | | | Uni-ZAP XR |

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|-------|--|--|------------------|-----------|---------|---------------|
| | excision | | | | | |
| S0348 | Cheek Carcinoma | Cheek Carcinoma | | | disease | pSport1 |
| S0350 | Pharynx Carcinoma | Pharynx carcinoma | Hypopharynx | | disease | pSport1 |
| S0352 | Larynx Carcinoma | Larynx carcinoma | | | disease | pSport1 |
| S0354 | Colon Normal II | Colon Normal | Colon | | | pSport1 |
| S0356 | Colon Carcinoma | Colon Carcinoma | Colon | | disease | pSport1 |
| S0358 | Colon Normal III | Colon Normal | Colon | | | pSport1 |
| S0360 | Colon Tumor II | Colon Tumor | Colon | | disease | pSport1 |
| S0362 | Human Gastrocnemius | Gastrocnemius muscle | | | | pSport1 |
| S0364 | Human Quadriceps | Quadriceps muscle | | | | pSport1 |
| S0366 | Human Soleus | Soleus Muscle | | | | pSport1 |
| S0368 | Human Pancreatic Langerhans | Islets of Langerhans | | | | pSport1 |
| S0370 | Larynx carcinoma II | Larynx carcinoma | | | disease | pSport1 |
| S0374 | Normal colon | Normal colon | | | | pSport1 |
| S0376 | Colon Tumor | Colon Tumor | | | disease | pSport1 |
| S0378 | Pancreas normal PCA4 No | Pancreas Normal PCA4 No | | | | pSport1 |
| S0380 | Pancreas Tumor PCA4 Tu | Pancreas Tumor PCA4 Tu | | | disease | pSport1 |
| S0384 | Tongue carcinoma | Tongue carcinoma | | | disease | pSport1 |
| S0386 | Human Whole Brain, re-excision | Whole brain | Brain | | | ZAP Express |
| S0388 | Human Hypothalamus, schizophrenia, re-excision | Human Hypothalamus, Schizophrenia | | | disease | Uni-ZAP XR |
| S0390 | Smooth muscle, control; re-excision | Smooth muscle | Pulmonary artery | Cell Line | | Uni-ZAP XR |
| S0392 | Salivary Gland | Salivary gland; normal | | | | pSport1 |
| S0400 | Brain; normal | Brain; normal | | | | pSport1 |
| S0404 | Rectum normal | Rectum, normal | | | | pSport1 |
| S0406 | Rectum tumour | Rectum tumour | | | | pSport1 |
| S0408 | Colon, normal | Colon, normal | | | | pSport1 |
| S0412 | Temporal cortex- Alzheimer; subtracted | Temporal cortex, alzheimer | | | disease | Other |
| S0414 | Hippocampus, Alzheimer Subtracted | Hippocampus, Alzheimer Subtracted | | | | Other |
| S0418 | CHME Cell Line; treated 5 hrs | CHME Cell Line; treated | | | | pCMVSPORT 3.0 |
| S0420 | CHME Cell Line, untreated | CHME Cell line, untreated | | | | pSport1 |
| S0422 | Mo7e Cell Line GM-CSF treated (1ng/ml) | Mo7e Cell Line GM-CSF treated (1ng/ml) | | | | pCMVSPORT 3.0 |
| S0424 | TF-1 Cell Line GM-CSF Treated | TF-1 Cell Line GM-CSF Treated | | | | pSport1 |
| S0426 | Monocyte activated; re-excision | Monocyte-activated | blood | Cell Line | | Uni-ZAP XR |
| S0428 | Neutrophils control; re- | human neutrophils | blood | Cell Line | | Uni-ZAP XR |

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|-------|-------------------------------------|-------------------------------------|------------------|-----------|---------|-----------------|
| | excision | | | | | |
| S0430 | Aryepiglottis Normal | Aryepiglottis Normal | | | | pSport1 |
| S0432 | Sinus piniformis Tumour | Sinus piniformis Tumour | | | | pSport1 |
| S0434 | Stomach Normal | Stomach Normal | | | disease | pSport1 |
| S0436 | Stomach Tumour | Stomach Tumour | | | disease | pSport1 |
| S0440 | Liver Tumour Met 5 Tu | Liver Tumour | | | | pSport1 |
| S0442 | Colon Normal | Colon Normal | | | | pSport1 |
| S0444 | Colon Tumor | Colon Tumour | | | disease | pSport1 |
| S0446 | Tongue Tumour | Tongue Tumour | | | | pSport1 |
| S0448 | Larynx Normal | Larynx Normal | | | | pSport1 |
| S0450 | Larynx Tumour | Larynx Tumour | | | | pSport1 |
| S0452 | Thymus | Thymus | | | | pSport1 |
| S0454 | Placenta | Placenta | Placenta | | | pSport1 |
| S0456 | Tongue Normal | Tongue Normal | | | | pSport1 |
| S0458 | Thyroid Normal (SDCA2 No) | Thyroid normal | | | | pSport1 |
| S0462 | Thyroid Thyroiditis | Thyroid Thyroiditis | | | | pSport1 |
| S0464 | Larynx Normal | Larynx Normal | | | | pSport1 |
| S0466 | Larynx Tumor | Larynx Tumor | | | disease | pSport1 |
| S0468 | Ea.hy.926 cell line | Ea.hy.926 cell line | | | | pSport1 |
| S0470 | Adenocarcinoma | PYFD | | | disease | pSport1 |
| S0472 | Lung Mesothelium | PYBT | | | | pSport1 |
| S0474 | Human blood platelets | Platelets | Blood platelets | | | Other |
| S0665 | Human Amygdala; re-excision | Amygdala | | | | Uni-ZAP XR |
| S3012 | Smooth Muscle Serum Treated, Norm | Smooth muscle | Pulmonary artery | Cell Line | | pBluescript |
| S3014 | Smooth muscle, serum induced,re-exc | Smooth muscle | Pulmonary artery | Cell Line | | pBluescript |
| S6014 | H. hypothalamus, frac A | Hypothalamus | Brain | | | ZAP Express |
| S6016 | H. Frontal Cortex, Epileptic | H. Brain, Frontal Cortex, Epileptic | Brain | | disease | Uni-ZAP XR |
| S6022 | H. Adipose Tissue | Human Adipose Tissue | | | | Uni-ZAP XR |
| S6024 | Alzheimers, spongy change | Alzheimer's/Spongy change | Brain | | disease | Uni-ZAP XR |
| S6026 | Frontal Lobe, Dementia | Frontal Lobe dementia/Alzheimer's | Brain | | | Uni-ZAP XR |
| S6028 | Human Manic Depression Tissue | Human Manic depression tissue | Brain | | disease | Uni-ZAP XR |
| T0002 | Activated T-cells | Activated T-Cell, PBL fraction | Blood | Cell Line | | pBluescript SK- |
| T0003 | Human Fetal Lung | Human Fetal Lung | | | | pBluescript SK- |
| T0004 | Human White Fat | Human White Fat | | | | pBluescript SK- |
| T0006 | Human Pineal Gland | Human Pinneal Gland | | | | pBluescript SK- |
| T0008 | Colorectal Tumor | Colorectal Tumor | | | disease | pBluescript SK- |
| T0010 | Human Infant Brain | Human Infant Brain | | | | Other |

| | | | | | | |
|-------|---|-----------------------------|--|--|---------|-----------------|
| T0023 | Human Pancreatic Carcinoma | Human Pancreatic Carcinoma | | | disease | pBluescript SK- |
| T0039 | HSA 172 Cells | Human HSA172 cell line | | | | pBluescript SK- |
| T0040 | HSC172 cells | SA172 Cells | | | | pBluescript SK- |
| T0041 | Jurkat T-cell G1 phase | Jurkat T-cell | | | | pBluescript SK- |
| T0042 | Jurkat T-Cell, S phase | Jurkat T-Cell Line | | | | pBluescript SK- |
| T0048 | Human Aortic Endothelium | Human Aortic Endothilium | | | | pBluescript SK- |
| T0049 | Aorta endothelial cells + TNF-a | Aorta endothelial cells | | | | pBluescript SK- |
| T0060 | Human White Adipose | Human White Fat | | | | pBluescript SK- |
| T0067 | Human Thyroid | Human Thyroid | | | | pBluescript SK- |
| T0068 | Normal Ovary, Premenopausal | Normal Ovary, Premenopausal | | | | pBluescript SK- |
| T0069 | Human Uterus, normal | Human Uterus, normal | | | | pBluescript SK- |
| T0071 | Human Bone Marrow | Human Bone Marrow | | | | pBluescript SK- |
| T0074 | Human Adult Retina | Human Adult Retina | | | | pBluescript SK- |
| T0079 | Human Kidney, normal Adult | Human Kidney, normal Adult | | | | pBluescript SK- |
| T0082 | Human Adult Retina | Human Adult Retina | | | | pBluescript SK- |
| T0103 | Human colon carcinoma (HCC) cell line | | | | | pBluescript SK- |
| T0104 | HCC cell line metastasis to liver | | | | | pBluescript SK- |
| T0109 | Human (HCC) cell line liver (mouse) metastasis, remake | | | | | pBluescript SK- |
| T0110 | Human colon carcinoma (HCC) cell line, remake | | | | | pBluescript SK- |
| T0114 | Human (Caco-2) cell line, adenocarcinoma, colon, remake | | | | | pBluescript SK- |
| T0115 | Human Colon Carcinoma (HCC) cell line | | | | | pBluescript SK- |
| L0002 | Atrium cDNA library Human heart | | | | | |
| L0005 | Clontech human aorta polyA+ mRNA (#6572) | | | | | |
| L0010 | GeneTrack, 4p16.3 JM Rommens | | | | | |
| L0021 | Human adult (K.Okubo) | | | | | |
| L0022 | Human adult lung 3" directed MboI cDNA | | | | | |
| L0034 | Human chromosome 14 | | | | | |
| L0040 | Human colon mucosa | | | | | |
| L0055 | Human promyelocyte | | | | | |
| L0060 | Human thymus NSTH II | | | | | |
| L0103 | DKFZphamy1 | amygdala | | | | |
| L0105 | Human aorta polyA+ | aorta | | | | |

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|-------|--|---------------------------------------|---------------|------------|--|-----------------|
| | (TFujiwara) | | | | | |
| L0119 | human glioblastoma library | brain | | | | |
| L0142 | Human placenta cDNA (TFujiwara) | placenta | | | | |
| L0143 | Human placenta polyA+ (TFujiwara) | placenta | | | | |
| L0157 | Human fetal brain (TFujiwara) | | brain | | | |
| L0163 | Human heart cDNA (YNakamura) | | heart | | | |
| L0183 | Human HeLa cells (M.Lovett) | | | HeLa | | |
| L0193 | Human osteosarcoma EGracia | osteosarcoma | | OsA-CL | | |
| L0194 | Human pancreatic cancer cell line Patu 8988t | pancreatic cancer | | Patu 8988t | | |
| L0351 | Infant brain, Bento Soares | | | | | BA, M13-derived |
| L0352 | Normalized infant brain, Bento Soares | | | | | BA, M13-derived |
| L0356 | S, Human foetal Adrenals tissue | | | | | Bluescript |
| L0361 | Stratagene ovary (#937217) | | ovary | | | Bluescript SK |
| L0362 | Stratagene ovarian cancer (#937219) | | | | | Bluescript SK- |
| L0363 | NCI_CGAP_GC2 | germ cell tumor | | | | Bluescript SK- |
| L0364 | NCI_CGAP_GC5 | germ cell tumor | | | | Bluescript SK- |
| L0366 | Stratagene schizo brain S11 | schizophrenic brain S-11 frontal lobe | | | | Bluescript SK- |
| L0367 | NCI_CGAP_Sch1 | Schwannoma tumor | | | | Bluescript SK- |
| L0368 | NCI_CGAP_SS1 | synovial sarcoma | | | | Bluescript SK- |
| L0369 | NCI_CGAP_AA1 | adrenal adenoma | adrenal gland | | | Bluescript SK- |
| L0370 | Johnston frontal cortex | pooled frontal lobe | brain | | | Bluescript SK- |
| L0371 | NCI_CGAP_Br3 | breast tumor | breast | | | Bluescript SK- |
| L0372 | NCI_CGAP_Co12 | colon tumor | colon | | | Bluescript SK- |
| L0373 | NCI_CGAP_Co11 | tumor | colon | | | Bluescript SK- |
| L0374 | NCI_CGAP_Co2 | tumor | colon | | | Bluescript SK- |
| L0375 | NCI_CGAP_Kid6 | kidney tumor | kidney | | | Bluescript SK- |
| L0376 | NCI_CGAP_Lar1 | larynx | larynx | | | Bluescript SK- |
| L0378 | NCI_CGAP_Lu1 | lung tumor | lung | | | Bluescript SK- |
| L0381 | NCI_CGAP_HN4 | squamous cell carcinoma | pharynx | | | Bluescript SK- |
| L0382 | NCI_CGAP_Pr25 | epithelium (cell line) | prostate | | | Bluescript SK- |
| L0383 | NCI_CGAP_Pr24 | invasive tumor (cell line) | prostate | | | Bluescript SK- |
| L0384 | NCI_CGAP_Pr23 | prostate tumor | prostate | | | Bluescript SK- |
| L0385 | NCI_CGAP_Gas1 | gastric tumor | stomach | | | Bluescript SK- |
| L0387 | NCI_CGAP_GCB0 | germinal center B-cells | tonsil | | | Bluescript SK- |
| L0388 | NCI_CGAP_HN6 | normal gingiva (cell | | | | Bluescript SK- |

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|-------|--|--|-------------|-------|--|---------------------------------------|
| | | line from immortalized kerati | | | | |
| L0389 | NCI_CGAP_HN5 | normal gingiva (cell line from primary keratinocyt | | | | Bluescript SK- |
| L0394 | H, Human adult Brain Cortex tissue | | | | | gt11 |
| L0411 | 1-NIB | | | | | Lafmid BA |
| L0435 | Infant brain, LLNL array of Dr. M. Soares 1NIB | | | | | lafmid BA |
| L0438 | normalized infant brain cDNA | total brain | brain | | | lafmid BA |
| L0439 | Soares infant brain 1NIB | | whole brain | | | Lafmid BA |
| L0441 | 2HB3MK | | | | | Lafmid BK |
| L0448 | 3HFLSK20 | | | | | Lafmid K |
| L0455 | Human retina cDNA randomly primed sublibrary | retina | eye | | | lambda gt10 |
| L0456 | Human retina cDNA Tsp509I-cleaved sublibrary | retina | eye | | | lambda gt10 |
| L0465 | TEST 1, Human adult Testis tissue | | | | | lambda nm1149 |
| L0471 | Human fetal heart, Lambda ZAP Express | | | | | Lambda ZAP Express |
| L0475 | KG1-a Lambda Zap Express cDNA library | | | KG1-a | | Lambda Zap Express (Stratagene) |
| L0477 | HPLA CCLee | placenta | | | | Lambda ZAP II |
| L0480 | Stratagene cat#937212 (1992) | | | | | Lambda ZAP, pBluescript SK(-) |
| L0481 | CD34+DIRECTIONAL | | | | | Lambda ZAPII |
| L0483 | Human pancreatic islet | | | | | Lambda ZAPII |
| L0485 | STRATAGENE Human skeletal muscle cDNA library, cat. #936215. | skeletal muscle | leg muscle | | | Lambda ZAPII |
| L0493 | NCI_CGAP_Ov26 | papillary serous carcinoma | ovary | | | pAMP1 |
| L0497 | NCI_CGAP_HSC4 | CD34+, CD38- from normal bone marrow donor | bone marrow | | | pAMP1 |
| L0498 | NCI_CGAP_HSC3 | CD34+, T negative, patient with chronic myelogenou | bone marrow | | | pAMP1 |
| L0500 | NCI_CGAP_Brn20 | oligodendroglioma | brain | | | pAMP1 |
| L0502 | NCI_CGAP_Br15 | adenocarcinoma | breast | | | pAMP1 |
| L0508 | NCI_CGAP_Lu25 | bronchioalveolar carcinoma | lung | | | pAMP1 |
| L0509 | NCI_CGAP_Lu26 | invasive adenocarcinoma | lung | | | pAMP1 |
| L0514 | NCI_CGAP_Ov31 | papillary serous carcinoma | ovary | | | pAMP1 |

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|-------|--------------------------------------|--|-------------|--|--|----------------|
| L0515 | NCI_CGAP_Ov32 | papillary serous carcinoma | ovary | | | pAMP1 |
| L0517 | NCI_CGAP_Pr1 | | | | | pAMP10 |
| L0518 | NCI_CGAP_Pr2 | | | | | pAMP10 |
| L0519 | NCI_CGAP_Pr3 | | | | | pAMP10 |
| L0520 | NCI_CGAP_Alv1 | alveolar rhabdomyosarcoma | | | | pAMP10 |
| L0521 | NCI_CGAP_Ew1 | Ewing's sarcoma | | | | pAMP10 |
| L0523 | NCI_CGAP_Lip2 | liposarcoma | | | | pAMP10 |
| L0525 | NCI_CGAP_Li2 | liver | | | | pAMP10 |
| L0526 | NCI_CGAP_Pr12 | metastatic prostate bone lesion | | | | pAMP10 |
| L0527 | NCI_CGAP_Ov2 | ovary | | | | pAMP10 |
| L0528 | NCI_CGAP_Pr5 | prostate | | | | pAMP10 |
| L0529 | NCI_CGAP_Pr6 | prostate | | | | pAMP10 |
| L0530 | NCI_CGAP_Pr8 | prostate | | | | pAMP10 |
| L0532 | NCI_CGAP_Thy1 | thyroid | | | | pAMP10 |
| L0533 | NCI_CGAP_HSC1 | stem cells | bone marrow | | | pAMP10 |
| L0536 | NCI_CGAP_Br4 | normal ductal tissue | breast | | | pAMP10 |
| L0540 | NCI_CGAP_Pr10 | invasive prostate tumor | prostate | | | pAMP10 |
| L0541 | NCI_CGAP_Pr7 | low-grade prostatic neoplasia | prostate | | | pAMP10 |
| L0542 | NCI_CGAP_Pr11 | normal prostatic epithelial cells | prostate | | | pAMP10 |
| L0543 | NCI_CGAP_Pr9 | normal prostatic epithelial cells | prostate | | | pAMP10 |
| L0544 | NCI_CGAP_Pr4 | prostatic intraepithelial neoplasia - high grade | prostate | | | pAMP10 |
| L0545 | NCI_CGAP_Pr4.1 | prostatic intraepithelial neoplasia - high grade | prostate | | | pAMP10 |
| L0546 | NCI_CGAP_Pr18 | stroma | prostate | | | pAMP10 |
| L0547 | NCI_CGAP_Pr16 | tumor | prostate | | | pAMP10 |
| L0549 | NCI_CGAP_HN10 | carcinoma in situ from retromolar trigone | | | | pAMP10 |
| L0557 | NCI_CGAP_Lu21 | small cell carcinoma | lung | | | pAMP10 |
| L0558 | NCI_CGAP_Ov40 | endometrioid ovarian metastasis | ovary | | | pAMP10 |
| L0561 | NCI_CGAP_HN11 | normal squamous epithelium | tongue | | | pAMP10 |
| L0563 | Human Bone Marrow Stromal Fibroblast | bone marrow | | | | pBluescript |
| L0564 | Jia bone marrow stroma | bone marrow stroma | | | | pBluescript |
| L0565 | Normal Human Trabecular Bone Cells | Bone | Hip | | | pBluescript |
| L0579 | Human fetal brain QBogin2 | cerebrum and cerebellum | | | | pBluescript SK |

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|-------|--|-------------------------|--------------------|---------|--|---------------------------------|
| L0581 | Stratagene liver (#937224) | | liver | | | pBluescript SK |
| L0584 | Stratagene cDNA library Human heart, cat#936208 | | | | | pBluescript SK(+) |
| L0586 | HTCDL1 | | | | | pBluescript SK(-) |
| L0587 | Stratagene colon HT29 (#937221) | | | | | pBluescript SK- |
| L0588 | Stratagene endothelial cell 937223 | | | | | pBluescript SK- |
| L0589 | Stratagene fetal retina 937202 | | | | | pBluescript SK- |
| L0590 | Stratagene fibroblast (#937212) | | | | | pBluescript SK- |
| L0591 | Stratagene HeLa cell s3 937216 | | | | | pBluescript SK- |
| L0592 | Stratagene hNT neuron (#937233) | | | | | pBluescript SK- |
| L0593 | Stratagene neuroepithelium (#937231) | | | | | pBluescript SK- |
| L0594 | Stratagene neuroepithelium NT2RAMI 937234 | | | | | pBluescript SK- |
| L0595 | Stratagene NT2 neuronal precursor 937230 | neuroepithelial cells | brain | | | pBluescript SK- |
| L0596 | Stratagene colon (#937204) | | colon | | | pBluescript SK- |
| L0597 | Stratagene corneal stroma (#937222) | | cornea | | | pBluescript SK- |
| L0598 | Morton Fetal Cochlea | cochlea | ear | | | pBluescript SK- |
| L0599 | Stratagene lung (#937210) | | lung | | | pBluescript SK- |
| L0600 | Weizmann Olfactory Epithelium | olfactory epithelium | nose | | | pBluescript SK- |
| L0601 | Stratagene pancreas (#937208) | | pancreas | | | pBluescript SK- |
| L0602 | Pancreatic Islet | pancreatic islet | pancreas | | | pBluescript SK- |
| L0603 | Stratagene placenta (#937225) | | placenta | | | pBluescript SK- |
| L0604 | Stratagene muscle 937209 | muscle | skeletal muscle | | | pBluescript SK- |
| L0605 | Stratagene fetal spleen (#937205) | fetal spleen | spleen | | | pBluescript SK- |
| L0606 | NCI_CGAP_Lym5 | follicular lymphoma | lymph node | | | pBluescript SK- |
| L0607 | NCI_CGAP_Lym6 | mantle cell lymphoma | lymph node | | | pBluescript SK- |
| L0608 | Stratagene lung carcinoma 937218 | lung carcinoma | lung | NCI-H69 | | pBluescript SK- |
| L0611 | Schiller meningioma | meningioma | brain | | | pBluescript SK- (Stratagene) |
| L0615 | 22 week old human fetal liver cDNA library | | | | | pBluescriptII SK(-) |
| L0617 | Chromosome 22 exon | | | | | pBluescriptIIKS + |

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|-------|----------------------|--|---------------------------|--|--|----------------------|
| L0618 | Chromosome 9 exon | | | | | pBluescriptIIKS + |
| L0619 | Chromosome 9 exon II | | | | | pBluescriptIIKS + |
| L0622 | HM1 | | | | | pcDNAII (Invitrogen) |
| L0623 | HM3 | pectoral muscle (after mastectomy) | | | | pcDNAII (Invitrogen) |
| L0625 | NCI_CGAP_AR1 | bulk alveolar tumor | | | | pCMV-SPORT2 |
| L0626 | NCI_CGAP_GC1 | bulk germ cell seminoma | | | | pCMV-SPORT2 |
| L0628 | NCI_CGAP_Ov1 | ovary bulk tumor | ovary | | | pCMV-SPORT2 |
| L0629 | NCI_CGAP_Mel3 | metastatic melanoma to bowel | bowel (skin primary) | | | pCMV-SPORT4 |
| L0630 | NCI_CGAP_CNS1 | substantia nigra | brain | | | pCMV-SPORT4 |
| L0631 | NCI_CGAP_Br7 | | breast | | | pCMV-SPORT4 |
| L0632 | NCI_CGAP_Li5 | hepatic adenoma | liver | | | pCMV-SPORT4 |
| L0634 | NCI_CGAP_Ov8 | serous adenocarcinoma | ovary | | | pCMV-SPORT4 |
| L0635 | NCI_CGAP_PNS1 | dorsal root ganglion | peripheral nervous system | | | pCMV-SPORT4 |
| L0636 | NCI_CGAP_Pit1 | four pooled pituitary adenomas | brain | | | pCMV-SPORT6 |
| L0637 | NCI_CGAP_Brn53 | three pooled meningiomas | brain | | | pCMV-SPORT6 |
| L0638 | NCI_CGAP_Brn35 | tumor, 5 pooled (see description) | brain | | | pCMV-SPORT6 |
| L0639 | NCI_CGAP_Brn52 | tumor, 5 pooled (see description) | brain | | | pCMV-SPORT6 |
| L0640 | NCI_CGAP_Br18 | four pooled high-grade tumors, including two prima | breast | | | pCMV-SPORT6 |
| L0641 | NCI_CGAP_Co17 | juvenile granulosa tumor | colon | | | pCMV-SPORT6 |
| L0642 | NCI_CGAP_Co18 | moderately differentiated adenocarcinoma | colon | | | pCMV-SPORT6 |
| L0643 | NCI_CGAP_Co19 | moderately differentiated adenocarcinoma | colon | | | pCMV-SPORT6 |
| L0644 | NCI_CGAP_Co20 | moderately differentiated adenocarcinoma | colon | | | pCMV-SPORT6 |
| L0645 | NCI_CGAP_Co21 | moderately differentiated adenocarcinoma | colon | | | pCMV-SPORT6 |
| L0646 | NCI_CGAP_Co14 | moderately-differentiated adenocarcinoma | colon | | | pCMV-SPORT6 |
| L0647 | NCI_CGAP_Sar4 | five pooled sarcomas, including myxoid liposarcoma | connective tissue | | | pCMV-SPORT6 |

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|-------|---------------------------|--|---------------------|--|--|--------------------------|
| L0648 | NCI_CGAP_Eso2 | squamous cell carcinoma | esophagus | | | pCMV-SPORT6 |
| L0649 | NCI_CGAP_GU1 | 2 pooled high-grade transitional cell tumors | genitourinary tract | | | pCMV-SPORT6 |
| L0650 | NCI_CGAP_Kid13 | 2 pooled Wilms" tumors, one primary and one metast | kidney | | | pCMV-SPORT6 |
| L0651 | NCI_CGAP_Kid8 | renal cell tumor | kidney | | | pCMV-SPORT6 |
| L0652 | NCI_CGAP_Lu27 | four pooled poorly-differentiated adenocarcinomas | lung | | | pCMV-SPORT6 |
| L0653 | NCI_CGAP_Lu28 | two pooled squamous cell carcinomas | lung | | | pCMV-SPORT6 |
| L0654 | NCI_CGAP_Lu31 | | lung, cell line | | | pCMV-SPORT6 |
| L0655 | NCI_CGAP_Lym12 | lymphoma, follicular mixed small and large cell | lymph node | | | pCMV-SPORT6 |
| L0656 | NCI_CGAP_Ov38 | normal epithelium | ovary | | | pCMV-SPORT6 |
| L0657 | NCI_CGAP_Ov23 | tumor, 5 pooled (see description) | ovary | | | pCMV-SPORT6 |
| L0658 | NCI_CGAP_Ov35 | tumor, 5 pooled (see description) | ovary | | | pCMV-SPORT6 |
| L0659 | NCI_CGAP_Pan1 | adenocarcinoma | pancreas | | | pCMV-SPORT6 |
| L0661 | NCI_CGAP_Mel15 | malignant melanoma, metastatic to lymph node | skin | | | pCMV-SPORT6 |
| L0662 | NCI_CGAP_Gas4 | poorly differentiated adenocarcinoma with signet r | stomach | | | pCMV-SPORT6 |
| L0663 | NCI_CGAP_Ut2 | moderately-differentiated endometrial adenocarcino | uterus | | | pCMV-SPORT6 |
| L0664 | NCI_CGAP_Ut3 | poorly-differentiated endometrial adenocarcinoma, | uterus | | | pCMV-SPORT6 |
| L0665 | NCI_CGAP_Ut4 | serous papillary carcinoma, high grade, 2 pooled t | uterus | | | pCMV-SPORT6 |
| L0666 | NCI_CGAP_Ut1 | well-differentiated endometrial adenocarcinoma, 7 | uterus | | | pCMV-SPORT6 |
| L0667 | NCI_CGAP_CML1 | myeloid cells, 18 pooled CML cases, BCR/ABL rearra | whole blood | | | pCMV-SPORT6 |
| L0684 | Stanley Frontal SB pool 1 | frontal lobe (see description) | brain | | | pCR2.1-TOPO (Invitrogen) |
| L0686 | Stanley Frontal SN pool 2 | frontal lobe (see description) | brain | | | pCR2.1-TOPO (Invitrogen) |
| L0697 | Testis 1 | | | | | PGEM 5zf(+) |

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|-------|------------------------------------|---------------|------------------|--|--|--|
| L0698 | Testis 2 | | | | | PGEM 5zf(+) |
| L0717 | Gessler Wilms tumor | | | | | pSPORT1 |
| L0731 | Soares_pregnant_uterus_NbHPU | | uterus | | | pT7T3-Pac |
| L0738 | Human colorectal cancer | | | | | pT7T3D |
| L0740 | Soares melanocyte 2NbHM | melanocyte | | | | pT7T3D (Pharmacia) with a modified polylinker |
| L0741 | Soares adult brain N2b4HB55Y | | brain | | | pT7T3D (Pharmacia) with a modified polylinker |
| L0742 | Soares adult brain N2b5HB55Y | | brain | | | pT7T3D (Pharmacia) with a modified polylinker |
| L0743 | Soares breast 2NbHBst | | breast | | | pT7T3D (Pharmacia) with a modified polylinker |
| L0744 | Soares breast 3NbHBst | | breast | | | pT7T3D (Pharmacia) with a modified polylinker |
| L0745 | Soares retina N2b4HR | retina | eye | | | pT7T3D (Pharmacia) with a modified polylinker |
| L0746 | Soares retina N2b5HR | retina | eye | | | pT7T3D (Pharmacia) with a modified polylinker |
| L0747 | Soares_fetal_heart_NbHH 19W | | heart | | | pT7T3D (Pharmacia) with a modified polylinker |
| L0748 | Soares fetal liver spleen 1NFLS | | Liver and Spleen | | | pT7T3D (Pharmacia) with a modified polylinker |
| L0749 | Soares_fetal_liver_spleen_1NFLS_S1 | | Liver and Spleen | | | pT7T3D (Pharmacia) with a modified polylinker |
| L0750 | Soares_fetal_lung_NbHL1 9W | | lung | | | pT7T3D (Pharmacia) with a modified polylinker |
| L0751 | Soares ovary tumor NbHOT | ovarian tumor | ovary | | | pT7T3D (Pharmacia) with a modified polylinker |

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| L0752 | Soares_parathyroid_tumor_NbHPA | parathyroid tumor | parathyroid gland | | | pT7T3D (Pharmacia) with a modified polylinker |
| L0753 | Soares_pineal_gland_N3H PG | | pineal gland | | | pT7T3D (Pharmacia) with a modified polylinker |
| L0754 | Soares_placenta Nb2HP | | placenta | | | pT7T3D (Pharmacia) with a modified polylinker |
| L0755 | Soares_placenta_8to9weeks_2NbHP8to9W | | placenta | | | pT7T3D (Pharmacia) with a modified polylinker |
| L0756 | Soares_multiple_sclerosis_2NbHMSP | multiple sclerosis lesions | | | | pT7T3D (Pharmacia) with a modified polylinker V_TYPE |
| L0757 | Soares_senescent_fibroblasts_NbHSF | senescent fibroblast | | | | pT7T3D (Pharmacia) with a modified polylinker V_TYPE |
| L0758 | Soares_testis_NHT | | | | | pT7T3D-Pac (Pharmacia) with a modified polylinker |
| L0759 | Soares_total_fetus_Nb2HF8_9w | | | | | pT7T3D-Pac (Pharmacia) with a modified polylinker |
| L0760 | Barstead aorta HPLRB3 | aorta | | | | pT7T3D-Pac (Pharmacia) with a modified polylinker |
| L0761 | NCI_CGAP_CLL1 | B-cell, chronic lymphocytic leukemia | | | | pT7T3D-Pac (Pharmacia) with a modified polylinker |
| L0762 | NCI_CGAP_Br1.1 | breast | | | | pT7T3D-Pac (Pharmacia) with a modified polylinker |
| L0763 | NCI_CGAP_Br2 | breast | | | | pT7T3D-Pac (Pharmacia) with a modified polylinker |
| L0764 | NCI_CGAP_Co3 | colon | | | | pT7T3D-Pac (Pharmacia) with a modified polylinker |

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| L0765 | NCI_CGAP_Co4 | colon | | | | pT7T3D-Pac (Pharmacia) with a modified polylinker |
| L0766 | NCI_CGAP_GCB1 | germinal center B cell | | | | pT7T3D-Pac (Pharmacia) with a modified polylinker |
| L0767 | NCI_CGAP_GC3 | pooled germ cell tumors | | | | pT7T3D-Pac (Pharmacia) with a modified polylinker |
| L0768 | NCI_CGAP_GC4 | pooled germ cell tumors | | | | pT7T3D-Pac (Pharmacia) with a modified polylinker |
| L0769 | NCI_CGAP_Brn25 | anaplastic oligodendroglioma | brain | | | pT7T3D-Pac (Pharmacia) with a modified polylinker |
| L0770 | NCI_CGAP_Brn23 | glioblastoma (pooled) | brain | | | pT7T3D-Pac (Pharmacia) with a modified polylinker |
| L0771 | NCI_CGAP_Co8 | adenocarcinoma | colon | | | pT7T3D-Pac (Pharmacia) with a modified polylinker |
| L0772 | NCI_CGAP_Co10 | colon tumor RER+ | colon | | | pT7T3D-Pac (Pharmacia) with a modified polylinker |
| L0773 | NCI_CGAP_Co9 | colon tumor RER+ | colon | | | pT7T3D-Pac (Pharmacia) with a modified polylinker |
| L0774 | NCI_CGAP_Kid3 | | kidney | | | pT7T3D-Pac (Pharmacia) with a modified polylinker |
| L0775 | NCI_CGAP_Kid5 | 2 pooled tumors (clear cell type) | kidney | | | pT7T3D-Pac (Pharmacia) with a modified polylinker |
| L0776 | NCI_CGAP_Lu5 | carcinoid | lung | | | pT7T3D-Pac (Pharmacia) with a modified polylinker |
| L0777 | Soares_NhHMPu_S1 | Pooled human melanocyte, fetal heart, and pregnant | mixed (see below) | | | pT7T3D-Pac (Pharmacia) with a modified polylinker |
| L0779 | Soares_NFL_T_GBC_S1 | | pooled | | | pT7T3D-Pac (Pharmacia) |

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|-------|-----------------------------|-------------------------|-------------|--|--|---|
| | | | | | | with a modified polylinker |
| L0780 | Soares_NSF_F8_9W_OT_PA_P_S1 | | pooled | | | pT7T3D-Pac (Pharmacia) with a modified polylinker |
| L0782 | NCI_CGAP_Pr21 | normal prostate | prostate | | | pT7T3D-Pac (Pharmacia) with a modified polylinker |
| L0783 | NCI_CGAP_Pr22 | normal prostate | prostate | | | pT7T3D-Pac (Pharmacia) with a modified polylinker |
| L0784 | NCI_CGAP_Lei2 | leiomyosarcoma | soft tissue | | | pT7T3D-Pac (Pharmacia) with a modified polylinker |
| L0785 | Barstead spleen HPLRB2 | | spleen | | | pT7T3D-Pac (Pharmacia) with a modified polylinker |
| L0786 | Soares_NbHFB | | whole brain | | | pT7T3D-Pac (Pharmacia) with a modified polylinker |
| L0787 | NCI_CGAP_Sub1 | | | | | pT7T3D-Pac (Pharmacia) with a modified polylinker |
| L0788 | NCI_CGAP_Sub2 | | | | | pT7T3D-Pac (Pharmacia) with a modified polylinker |
| L0789 | NCI_CGAP_Sub3 | | | | | pT7T3D-Pac (Pharmacia) with a modified polylinker |
| L0790 | NCI_CGAP_Sub4 | | | | | pT7T3D-Pac (Pharmacia) with a modified polylinker |
| L0791 | NCI_CGAP_Sub5 | | | | | pT7T3D-Pac (Pharmacia) with a modified polylinker |
| L0792 | NCI_CGAP_Sub6 | | | | | pT7T3D-Pac (Pharmacia) with a modified polylinker |
| L0794 | NCI_CGAP_GC6 | pooled germ cell tumors | | | | pT7T3D-Pac (Pharmacia) with a modified polylinker |

| | | | | | | |
|-------|-----------------------------------|---|----------|--|--|--|
| L0796 | NCI_CGAP_Brn50 | medulloblastoma | brain | | | pT7T3D-Pac (Pharmacia) with a modified polylinker |
| L0800 | NCI_CGAP_Co16 | colon tumor, RER+ | colon | | | pT7T3D-Pac (Pharmacia) with a modified polylinker |
| L0803 | NCI_CGAP_Kid11 | | kidney | | | pT7T3D-Pac (Pharmacia) with a modified polylinker |
| L0804 | NCI_CGAP_Kid12 | 2 pooled tumors (clear cell type) | kidney | | | pT7T3D-Pac (Pharmacia) with a modified polylinker |
| L0805 | NCI_CGAP_Lu24 | carcinoid | lung | | | pT7T3D-Pac (Pharmacia) with a modified polylinker |
| L0806 | NCI_CGAP_Lu19 | squamous cell carcinoma, poorly differentiated (4 | lung | | | pT7T3D-Pac (Pharmacia) with a modified polylinker |
| L0807 | NCI_CGAP_Ov18 | fibrotheoma | ovary | | | pT7T3D-Pac (Pharmacia) with a modified polylinker |
| L0808 | Barstead prostate BPH HPLRB4 1 | | prostate | | | pT7T3D-Pac (Pharmacia) with a modified polylinker |
| L0809 | NCI_CGAP_Pr28 | | prostate | | | pT7T3D-Pac (Pharmacia) with a modified polylinker |
| L2250 | Human cerebral cortex | cerebral cortex | | | | |
| L2251 | Human fetal lung | Fetal lung | | | | |

TABLE 5

| OMIM Reference | Description |
|----------------|---|
| 103050 | Autism, succinylpurinemic |
| 103050 | Adenylosuccinase deficiency |
| 104770 | Amyloidosis, secondary, susceptibility to |
| 106180 | Myocardial infarction, susceptibility to |
| 107670 | Apolipoprotein A-II deficiency |
| 108725 | Atherosclerosis, susceptibility to |
| 109690 | Asthma, nocturnal, susceptibility to |
| 109690 | Obesity, susceptibility to |
| 110700 | Vivax malaria, susceptibility to |
| 114290 | Campomelic dysplasia with autosomal sex reversal |
| 115660 | Cataract, cerulean, type 1 |
| 116860 | Cavernous angiomatous malformations |
| 120700 | C3 deficiency |
| 121050 | Contractural arachnodactyly, congenital |
| 123101 | Craniosynostosis, type 2 |
| 124030 | Parkinsonism, susceptibility to |
| 124030 | Debrisoquine sensitivity |
| 126150 | Diphtheria, susceptibility to |
| 126337 | Myxoid liposarcoma |
| 126650 | Chloride diarrhea, congenital, Finnish type, 214700 |
| 126650 | Colon cancer |
| 129900 | EEC syndrome-1 |
| 133170 | Erythremia |
| 133171 | [Erythrocytosis, familial], 133100 |
| 135940 | Ichthyosis vulgaris, 146700 |
| 136836 | Fucosyltransferase-6 deficiency |
| 138033 | Diabetes mellitus, type II |
| 138700 | [Apolipoprotein H deficiency] |
| 138981 | Pulmonary alveolar proteinosis, 265120 |
| 139190 | Gigantism due to GHRF hypersecretion |
| 139190 | Isolated growth hormone deficiency due to defect in GHRF |
| 139250 | Isolated growth hormone deficiency, Illig type with absent GH and Kowarski type with bioinactive GH |
| 141750 | Alpha-thalassemia/mental retardation syndrome, type 1 |
| 141800 | Methemoglobinemias, alpha- |
| 141800 | Thalassemias, alpha- |
| 141800 | Erythremias, alpha- |
| 141800 | Heinz body anemias, alpha- |
| 141850 | Thalassemia, alpha- |
| 141850 | Erythrocytosis |
| 141850 | Heinz body anemia |
| 141850 | Hemoglobin H disease |
| 141850 | Hypochromic microcytic anemia |

| | |
|--------|--|
| 145001 | Hyperparathyroidism-jaw tumor syndrome |
| 145981 | Hypocalciuric hypercalcemia, type II |
| 146790 | Lupus nephritis, susceptibility to |
| 147141 | Leukemia, acute lymphoblastic |
| 148500 | Tylosis with esophageal cancer |
| 150200 | [Placental lactogen deficiency] |
| 152445 | Vohwinkel syndrome, 124500 |
| 152445 | Erythrokeratoderma, progressive symmetric, 602036 |
| 154275 | Malignant hyperthermia susceptibility 2 |
| 154276 | Malignant hyperthermia susceptibility 3 |
| 156850 | Cataract, congenital, with microphthalmia |
| 159000 | Muscular dystrophy, limb-girdle, type 1A |
| 159001 | Muscular dystrophy, limb-girdle, type 1B |
| 162100 | Neuralgic amyotrophy with predilection for brachial plexus |
| 164953 | Liposarcoma |
| 170500 | Myotonia congenita, atypical acetazolamide-responsive |
| 170500 | Paramyotonia congenita, 168300 |
| 170500 | Hyperkalemic periodic paralysis |
| 173360 | Thrombophilia due to excessive plasminogen activator inhibitor |
| 173360 | Hemorrhagic diathesis due to PAI1 deficiency |
| 174000 | Medullary cystic kidney disease, AD |
| 174900 | Polyposis, juvenile intestinal |
| 176960 | Pituitary tumor, invasive |
| 179095 | Male infertility |
| 179755 | Renal cell carcinoma, papillary, 1 |
| 180071 | Retinitis pigmentosa, autosomal recessive |
| 180860 | Russell-Silver syndrome |
| 182380 | Glucose/galactose malabsorption |
| 182452 | Lung cancer, small cell |
| 182860 | Pyropoikilocytosis |
| 182860 | Spherocytosis, recessive |
| 182860 | Elliptocytosis-2 |
| 186580 | Arthrocutaneousveal granulomatosis |
| 188070 | Bleeding disorder due to defective thromboxane A2 receptor |
| 188826 | Sorsby fundus dystrophy, 136900 |
| 190040 | Dermatofibrosarcoma protuberans |
| 190040 | Giant-cell fibroblastoma |
| 190040 | Meningioma, SIS-related |
| 191092 | Tuberous sclerosis-2 |
| 191315 | Insensitivity to pain, congenital, with anhidrosis, 256800 |
| 192974 | Neonatal alloimmune thrombocytopenia |
| 192974 | Glycoprotein Ia deficiency |
| 224100 | Congenital dyserythropoietic anemia II |
| 230200 | Galactokinase deficiency with cataracts |
| 230800 | Gaucher disease |
| 230800 | Gaucher disease with cardiovascular calcification |

| | |
|--------|---|
| 236730 | Urofacial syndrome |
| 249000 | Meckel syndrome |
| 253250 | Mulibrey nanism |
| 264470 | Adrenoleukodystrophy, pseudoneonatal |
| 266200 | Anemia, hemolytic, due to PK deficiency |
| 600140 | Rubenstein-Taybi syndrome, 180849 |
| 600194 | Ichthyosis bullosa of Siemens, 146800 |
| 600231 | Palmoplantar keratoderma, Bothnia type |
| 600273 | Polycystic kidney disease, infantile severe, with tuberous sclerosis |
| 600281 | Non-insulin-dependent diabetes mellitus, 125853 |
| 600281 | MODY, type 1, 125850 |
| 600584 | Atrial septal defect with atrioventricular conduction defects, 108900 |
| 600808 | Enuresis, nocturnal, 2 |
| 600897 | Cataract, zonular pulverulent-1, 116200 |
| 600957 | Persistent Mullerian duct syndrome, type I, 261550 |
| 601002 | 5-oxoprolinuria, 266130 |
| 601002 | Hemolytic anemia due to glutathione synthetase deficiency, 231900 |
| 601105 | Pycnodysostosis, 265800 |
| 601146 | Brachydactyly, type C, 113100 |
| 601146 | Acromesomelic dysplasia, Hunter-Thompson type, 201250 |
| 601146 | Chondrodysplasia, Grebe type, 200700 |
| 601238 | Cerebellar ataxia, Cayman type |
| 601284 | Hereditary hemorrhagic telangiectasia-2, 600376 |
| 601313 | Polycystic kidney disease, adult type I, 173900 |
| 601412 | Deafness, autosomal dominant 7 |
| 601493 | Cardiomyopathy, dilated 1C |
| 601596 | Charcot-Marie-Tooth neuropathy, demyelinating |
| 601652 | Glaucoma 1A, primary open angle, juvenile-onset, 137750 |
| 601769 | Osteoporosis, involutional |
| 601769 | Rickets, vitamin D-resistant, 277440 |
| 601785 | Carbohydrate-deficient glycoprotein syndrome, type I, 212065 |
| 601846 | Muscular dystrophy with rimmed vacuoles |
| 602116 | Glioma |
| 602136 | Refsum disease, infantile, 266510 |
| 602136 | Zellweger syndrome-1, 214100 |
| 602136 | Adrenoleukodystrophy, neonatal, 202370 |
| 602216 | Peutz-Jeghers syndrome, 175200 |
| 602447 | Coronary artery disease, susceptibility to |
| 602477 | Febrile convulsions, familial, 2 |
| 602491 | Hyperlipidemia, familial combined, 1 |
| 602782 | Faisalabad histiocytosis |

Polynucleotide and Polypeptide Variants

[98] The present invention is directed to variants of the polynucleotide sequence disclosed in SEQ ID NO:X or the complementary strand thereto, nucleotide sequences encoding the polypeptide of SEQ ID NO:Y, the nucleotide sequence of SEQ ID NO:X encoding the polypeptide sequence as defined in column 7 of Table 1A, nucleotide sequences encoding the polypeptide as defined in column 7 of Table 1A, the nucleotide sequence as defined in columns 8 and 9 of Table 2, nucleotide sequences encoding the polypeptide encoded by the nucleotide sequence as defined in columns 8 and 9 of Table 2, the nucleotide sequence as defined in column 6 of Table 1B, nucleotide sequences encoding the polypeptide encoded by the nucleotide sequence as defined in column 6 of Table 1B, the cDNA sequence contained in Clone ID NO:Z, and/or nucleotide sequences encoding the polypeptide encoded by the cDNA sequence contained in Clone ID NO:Z.

[99] The present invention also encompasses variants of the polypeptide sequence disclosed in SEQ ID NO:Y, the polypeptide sequence as defined in column 7 of Table 1A, a polypeptide sequence encoded by the polynucleotide sequence in SEQ ID NO:X, a polypeptide sequence encoded by the nucleotide sequence as defined in columns 8 and 9 of Table 2, a polypeptide sequence encoded by the nucleotide sequence as defined in column 6 of Table 1B, a polypeptide sequence encoded by the complement of the polynucleotide sequence in SEQ ID NO:X, and/or a polypeptide sequence encoded by the cDNA sequence contained in Clone ID NO:Z.

[100] "Variant" refers to a polynucleotide or polypeptide differing from the polynucleotide or polypeptide of the present invention, but retaining essential properties thereof. Generally, variants are overall closely similar, and, in many regions, identical to the polynucleotide or polypeptide of the present invention.

[101] Thus, one aspect of the invention provides an isolated nucleic acid molecule comprising, or alternatively consisting of, a polynucleotide having a nucleotide sequence selected from the group consisting of: (a) a nucleotide sequence described in SEQ ID NO:X or contained in the cDNA sequence of Clone ID NO:Z; (b) a nucleotide sequence in SEQ ID NO:X or the cDNA in Clone ID NO:Z which encodes the complete amino acid sequence of SEQ ID NO:Y or the complete amino acid sequence encoded by the cDNA in Clone ID NO:Z; (c) a nucleotide sequence in SEQ ID NO:X or the cDNA in Clone ID NO:Z which encodes a mature polypeptide; (d) a nucleotide sequence in SEQ ID NO:X or the cDNA sequence of Clone ID NO:Z, which encodes a biologically active fragment of a polypeptide; (e) a nucleotide sequence in SEQ ID NO:X or the cDNA sequence of Clone ID NO:Z, which

encodes an antigenic fragment of a polypeptide; (f) a nucleotide sequence encoding a polypeptide comprising the complete amino acid sequence of SEQ ID NO:Y or the complete amino acid sequence encoded by the cDNA in Clone ID NO:Z; (g) a nucleotide sequence encoding a mature polypeptide of the amino acid sequence of SEQ ID NO:Y or the amino acid sequence encoded by the cDNA in Clone ID NO:Z; (h) a nucleotide sequence encoding a biologically active fragment of a polypeptide having the complete amino acid sequence of SEQ ID NO:Y or the complete amino acid sequence encoded by the cDNA in Clone ID NO:Z; (i) a nucleotide sequence encoding an antigenic fragment of a polypeptide having the complete amino acid sequence of SEQ ID NO:Y or the complete amino acid sequence encoded by the cDNA in Clone ID NO:Z; and (j) a nucleotide sequence complementary to any of the nucleotide sequences in (a), (b), (c), (d), (e), (f), (g), (h), or (i) above.

[102] The present invention is also directed to nucleic acid molecules which comprise, or alternatively consist of, a nucleotide sequence which is at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99% or 100%, identical to, for example, any of the nucleotide sequences in (a), (b), (c), (d), (e), (f), (g), (h), (i), or (j) above, the nucleotide coding sequence in SEQ ID NO:X or the complementary strand thereto, the nucleotide coding sequence of the cDNA contained in Clone ID NO:Z or the complementary strand thereto, a nucleotide sequence encoding the polypeptide of SEQ ID NO:Y, a nucleotide sequence encoding a polypeptide sequence encoded by the nucleotide sequence in SEQ ID NO:X, a polypeptide sequence encoded by the complement of the polynucleotide sequence in SEQ ID NO:X, a nucleotide sequence encoding the polypeptide encoded by the cDNA contained in Clone ID NO:Z, the nucleotide coding sequence in SEQ ID NO:X as defined in columns 8 and 9 of Table 2 or the complementary strand thereto, a nucleotide sequence encoding the polypeptide encoded by the nucleotide sequence in SEQ ID NO:X as defined in columns 8 and 9 of Table 2 or the complementary strand thereto, the nucleotide coding sequence in SEQ ID NO:B as defined in column 6 of Table 1B or the complementary strand thereto, a nucleotide sequence encoding the polypeptide encoded by the nucleotide sequence in SEQ ID NO:B as defined in column 6 of Table 1B or the complementary strand thereto, the nucleotide sequence in SEQ ID NO:X encoding the polypeptide sequence as defined in column 7 of Table 1A or the complementary strand thereto, nucleotide sequences encoding the polypeptide as defined in column 7 of Table 1A or the complementary strand thereto, and/or polynucleotide fragments of any of these nucleic acid molecules (e.g., those fragments described herein). Polynucleotides which hybridize to the complement of these nucleic acid molecules under stringent hybridization

conditions or alternatively, under lower stringency conditions, are also encompassed by the invention, as are polypeptides encoded by these polynucleotides and nucleic acids.

[103] In a preferred embodiment, the invention encompasses nucleic acid molecules which comprise, or alternatively, consist of a polynucleotide which hybridizes under stringent hybridization conditions, or alternatively, under lower stringency conditions, to a polynucleotide in (a), (b), (c), (d), (e), (f), (g), (h), or (i), above, as are polypeptides encoded by these polynucleotides. In another preferred embodiment, polynucleotides which hybridize to the complement of these nucleic acid molecules under stringent hybridization conditions, or alternatively, under lower stringency conditions, are also encompassed by the invention, as are polypeptides encoded by these polynucleotides.

[104] In another embodiment, the invention provides a purified protein comprising, or alternatively consisting of, a polypeptide having an amino acid sequence selected from the group consisting of: (a) the complete amino acid sequence of SEQ ID NO:Y or the complete amino acid sequence encoded by the cDNA in Clone ID NO:Z; (b) the amino acid sequence of a mature form of a polypeptide having the amino acid sequence of SEQ ID NO:Y or the amino acid sequence encoded by the cDNA in Clone ID NO:Z; (c) the amino acid sequence of a biologically active fragment of a polypeptide having the complete amino acid sequence of SEQ ID NO:Y or the complete amino acid sequence encoded by the cDNA in Clone ID NO:Z; and (d) the amino acid sequence of an antigenic fragment of a polypeptide having the complete amino acid sequence of SEQ ID NO:Y or the complete amino acid sequence encoded by the cDNA in Clone ID NO:Z.

[105] The present invention is also directed to proteins which comprise, or alternatively consist of, an amino acid sequence which is at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99% or 100%, identical to, for example, any of the amino acid sequences in (a), (b), (c), or (d), above, the amino acid sequence shown in SEQ ID NO:Y, the amino acid sequence encoded by the cDNA contained in Clone ID NO:Z, the amino acid sequence of the polypeptide encoded by the nucleotide sequence in SEQ ID NO:X as defined in columns 8 and 9 of Table 2, the amino acid sequence of the polypeptide encoded by the nucleotide sequence in SEQ ID NO:B as defined in column 6 of Table 1B, the amino acid sequence as defined in column 7 of Table 1A, an amino acid sequence encoded by the nucleotide sequence in SEQ ID NO:X, and an amino acid sequence encoded by the complement of the polynucleotide sequence in SEQ ID NO:X. Fragments of these polypeptides are also provided (e.g., those fragments described herein). Further proteins encoded by

polynucleotides which hybridize to the complement of the nucleic acid molecules encoding these amino acid sequences under stringent hybridization conditions or alternatively, under lower stringency conditions, are also encompassed by the invention, as are the polynucleotides encoding these proteins.

[106] By a nucleic acid having a nucleotide sequence at least, for example, 95% "identical" to a reference nucleotide sequence of the present invention, it is intended that the nucleotide sequence of the nucleic acid is identical to the reference sequence except that the nucleotide sequence may include up to five point mutations per each 100 nucleotides of the reference nucleotide sequence encoding the polypeptide. In other words, to obtain a nucleic acid having a nucleotide sequence at least 95% identical to a reference nucleotide sequence, up to 5% of the nucleotides in the reference sequence may be deleted or substituted with another nucleotide, or a number of nucleotides up to 5% of the total nucleotides in the reference sequence may be inserted into the reference sequence. The query sequence may be an entire sequence referred to in Table 1A or 2 as the ORF (open reading frame), or any fragment specified as described herein.

[107] As a practical matter, whether any particular nucleic acid molecule or polypeptide is at least 80%, 85%, 90%, 95%, 96%, 97%, 98% or 99% identical to a nucleotide sequence of the present invention can be determined conventionally using known computer programs. A preferred method for determining the best overall match between a query sequence (a sequence of the present invention) and a subject sequence, also referred to as a global sequence alignment, can be determined using the FASTDB computer program based on the algorithm of Brutlag et al. (Comp. App. Biosci. 6:237-245 (1990)). In a sequence alignment the query and subject sequences are both DNA sequences. An RNA sequence can be compared by converting U's to T's. The result of said global sequence alignment is expressed as percent identity. Preferred parameters used in a FASTDB alignment of DNA sequences to calculate percent identity are: Matrix=Unitary, k-tuple=4, Mismatch Penalty=1, Joining Penalty=30, Randomization Group Length=0, Cutoff Score=1, Gap Penalty=5, Gap Size Penalty 0.05, Window Size=500 or the length of the subject nucleotide sequence, whichever is shorter.

[108] If the subject sequence is shorter than the query sequence because of 5' or 3' deletions, not because of internal deletions, a manual correction must be made to the results. This is because the FASTDB program does not account for 5' and 3' truncations of the subject sequence when calculating percent identity. For subject sequences truncated at the 5'

or 3' ends, relative to the query sequence, the percent identity is corrected by calculating the number of bases of the query sequence that are 5' and 3' of the subject sequence, which are not matched/aligned, as a percent of the total bases of the query sequence. Whether a nucleotide is matched/aligned is determined by results of the FASTDB sequence alignment. This percentage is then subtracted from the percent identity, calculated by the above FASTDB program using the specified parameters, to arrive at a final percent identity score. This corrected score is what is used for the purposes of the present invention. Only bases outside the 5' and 3' bases of the subject sequence, as displayed by the FASTDB alignment, which are not matched/aligned with the query sequence, are calculated for the purposes of manually adjusting the percent identity score.

[109] For example, a 90 base subject sequence is aligned to a 100 base query sequence to determine percent identity. The deletions occur at the 5' end of the subject sequence and therefore, the FASTDB alignment does not show a matched/alignment of the first 10 bases at 5' end. The 10 unpaired bases represent 10% of the sequence (number of bases at the 5' and 3' ends not matched/total number of bases in the query sequence) so 10% is subtracted from the percent identity score calculated by the FASTDB program. If the remaining 90 bases were perfectly matched the final percent identity would be 90%. In another example, a 90 base subject sequence is compared with a 100 base query sequence. This time the deletions are internal deletions so that there are no bases on the 5' or 3' of the subject sequence which are not matched/aligned with the query. In this case the percent identity calculated by FASTDB is not manually corrected. Once again, only bases 5' and 3' of the subject sequence which are not matched/aligned with the query sequence are manually corrected for. No other manual corrections are to be made for the purposes of the present invention.

[110] By a polypeptide having an amino acid sequence at least, for example, 95% "identical" to a query amino acid sequence of the present invention, it is intended that the amino acid sequence of the subject polypeptide is identical to the query sequence except that the subject polypeptide sequence may include up to five amino acid alterations per each 100 amino acids of the query amino acid sequence. In other words, to obtain a polypeptide having an amino acid sequence at least 95% identical to a query amino acid sequence, up to 5% of the amino acid residues in the subject sequence may be inserted, deleted, (indels) or substituted with another amino acid. These alterations of the reference sequence may occur at the amino or carboxy terminal positions of the reference amino acid sequence or anywhere between those terminal positions, interspersed either individually among residues in the

reference sequence or in one or more contiguous groups within the reference sequence.

[111] As a practical matter, whether any particular polypeptide is at least 80%, 85%, 90%, 95%, 96%, 97%, 98% or 99% identical to, for instance, the amino acid sequence of a polypeptide referred to in Table 1A (e.g., the amino acid sequence identified in column 6) or Table 2 (e.g., the amino acid sequence of the polypeptide encoded by the polynucleotide sequence defined in columns 8 and 9 of Table 2) or a fragment thereof, the amino acid sequence of the polypeptide encoded by the polynucleotide sequence in SEQ ID NO:B as defined in column 6 of Table 1B or a fragment thereof, the amino acid sequence of the polypeptide encoded by the nucleotide sequence in SEQ ID NO:X or a fragment thereof, or the amino acid sequence of the polypeptide encoded by cDNA contained in Clone ID NO:Z, or a fragment thereof, can be determined conventionally using known computer programs. A preferred method for determining the best overall match between a query sequence (a sequence of the present invention) and a subject sequence, also referred to as a global sequence alignment, can be determined using the FASTDB computer program based on the algorithm of Brutlag et al. (Comp. App. Biosci.6:237-245 (1990)). In a sequence alignment the query and subject sequences are either both nucleotide sequences or both amino acid sequences. The result of said global sequence alignment is expressed as percent identity. Preferred parameters used in a FASTDB amino acid alignment are: Matrix=PAM 0, k-tuple=2, Mismatch Penalty=1, Joining Penalty=20, Randomization Group Length=0, Cutoff Score=1, Window Size=sequence length, Gap Penalty=5, Gap Size Penalty=0.05, Window Size=500 or the length of the subject amino acid sequence, whichever is shorter.

[112] If the subject sequence is shorter than the query sequence due to N- or C-terminal deletions, not because of internal deletions, a manual correction must be made to the results. This is because the FASTDB program does not account for N- and C-terminal truncations of the subject sequence when calculating global percent identity. For subject sequences truncated at the N- and C-termini, relative to the query sequence, the percent identity is corrected by calculating the number of residues of the query sequence that are N- and C-terminal of the subject sequence, which are not matched/aligned with a corresponding subject residue, as a percent of the total bases of the query sequence. Whether a residue is matched/aligned is determined by results of the FASTDB sequence alignment. This percentage is then subtracted from the percent identity, calculated by the above FASTDB program using the specified parameters, to arrive at a final percent identity score. This final percent identity score is what is used for the purposes of the present invention. Only residues

to the N- and C-termini of the subject sequence, which are not matched/aligned with the query sequence, are considered for the purposes of manually adjusting the percent identity score. That is, only query residue positions outside the farthest N- and C- terminal residues of the subject sequence.

[113] For example, a 90 amino acid residue subject sequence is aligned with a 100 residue query sequence to determine percent identity. The deletion occurs at the N-terminus of the subject sequence and therefore, the FASTDB alignment does not show a matching/alignment of the first 10 residues at the N-terminus. The 10 unpaired residues represent 10% of the sequence (number of residues at the N- and C- termini not matched/total number of residues in the query sequence) so 10% is subtracted from the percent identity score calculated by the FASTDB program. If the remaining 90 residues were perfectly matched the final percent identity would be 90%. In another example, a 90 residue subject sequence is compared with a 100 residue query sequence. This time the deletions are internal deletions so there are no residues at the N- or C-termini of the subject sequence which are not matched/aligned with the query. In this case the percent identity calculated by FASTDB is not manually corrected. Once again, only residue positions outside the N- and C-terminal ends of the subject sequence, as displayed in the FASTDB alignment, which are not matched/aligned with the query sequence are manually corrected for. No other manual corrections are to be made for the purposes of the present invention.

[114] The polynucleotide variants of the invention may contain alterations in the coding regions, non-coding regions, or both. Especially preferred are polynucleotide variants containing alterations which produce silent substitutions, additions, or deletions, but do not alter the properties or activities of the encoded polypeptide. Nucleotide variants produced by silent substitutions due to the degeneracy of the genetic code are preferred. Moreover, polypeptide variants in which less than 50, less than 40, less than 30, less than 20, less than 10, or 5-50, 5-25, 5-10, 1-5, or 1-2 amino acids are substituted, deleted, or added in any combination are also preferred. Polynucleotide variants can be produced for a variety of reasons, e.g., to optimize codon expression for a particular host (change codons in the human mRNA to those preferred by a bacterial host such as *E. coli*).

[115] Naturally occurring variants are called "allelic variants," and refer to one of several alternate forms of a gene occupying a given locus on a chromosome of an organism. (Genes II, Lewin, B., ed., John Wiley & Sons, New York (1985)). These allelic variants can vary at either the polynucleotide and/or polypeptide level and are included in the present invention.